

# **Foundational advances in RNA engineering applied to control of biosynthesis**

Christina D. Smolke

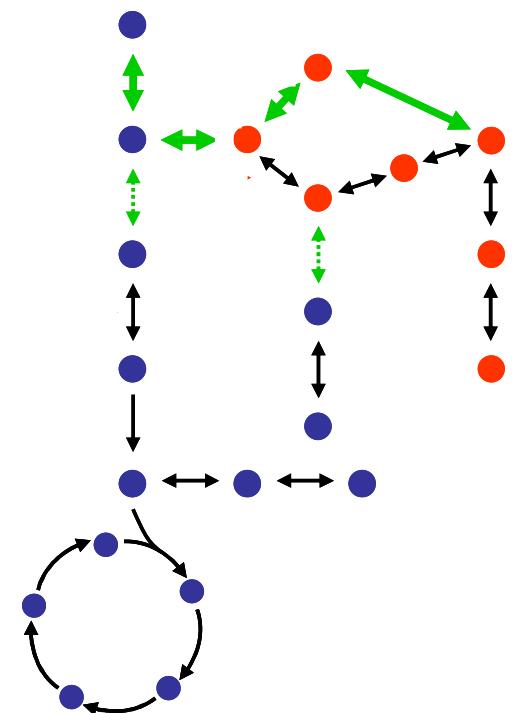
Division of Chemistry and Chemical Engineering  
California Institute of Technology

February 11, 2008

MEWG: Interagency Conference on Metabolic Engineering

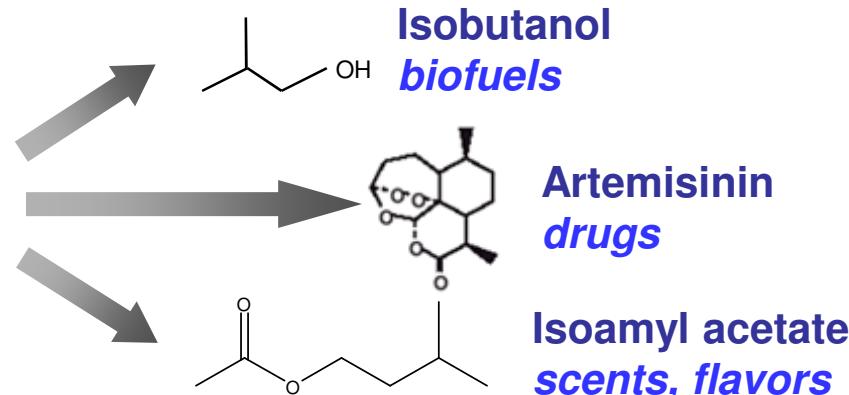
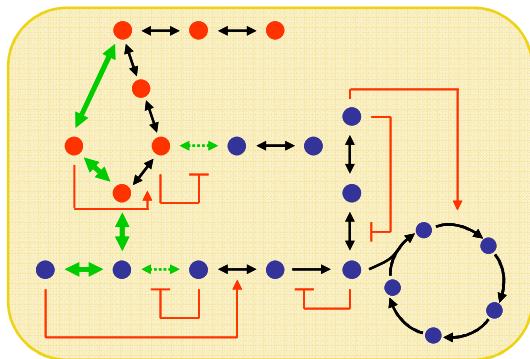


# The role of feedback control in biosynthesis

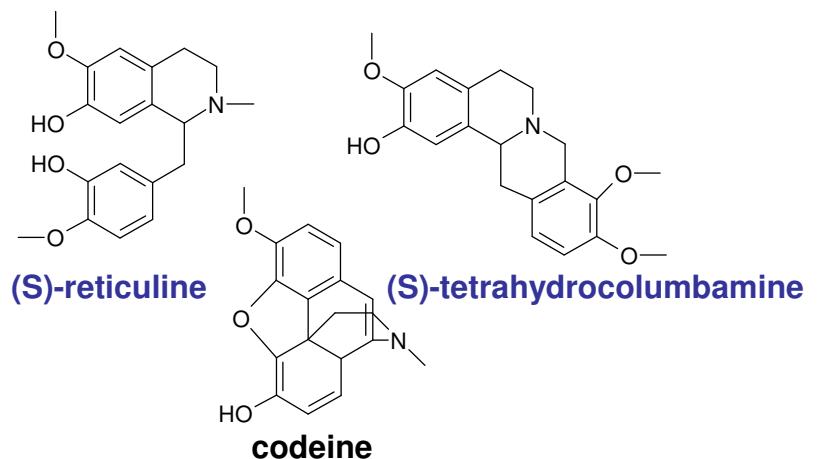


# Applications of engineered biological systems

## Metabolic engineering



## Benzylisoquinoline alkaloid biosynthesis

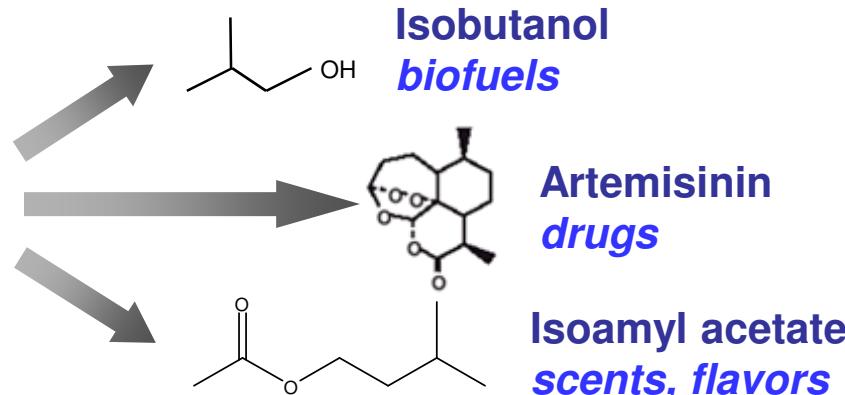
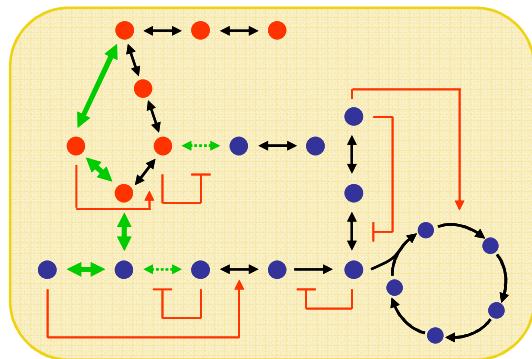


*Papaver somniferum* (opium poppy)

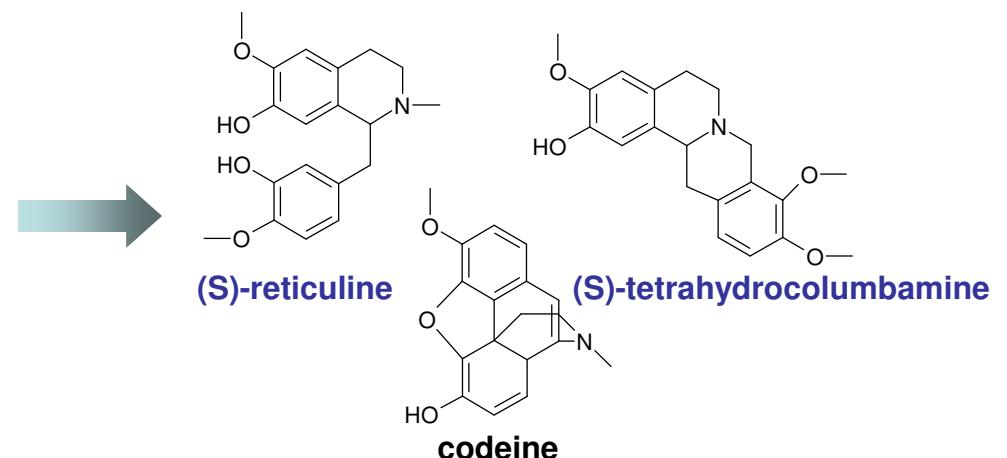
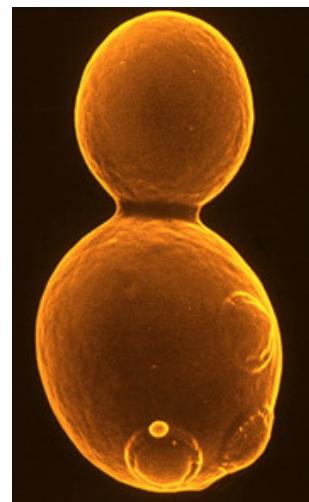
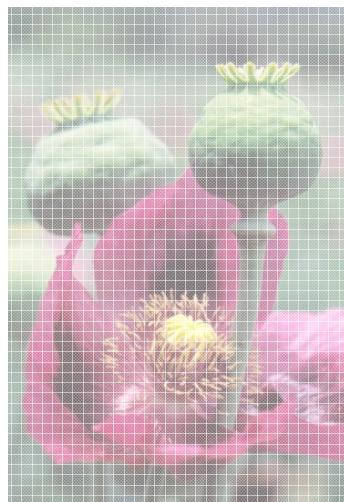
<http://www.nature.com/news/2004/040816/images/yeast.jpg>  
<http://www.westwindphotos.ca/images/101%20Opium%20Poppy.jpg>

# Applications of engineered biological systems

## Metabolic engineering

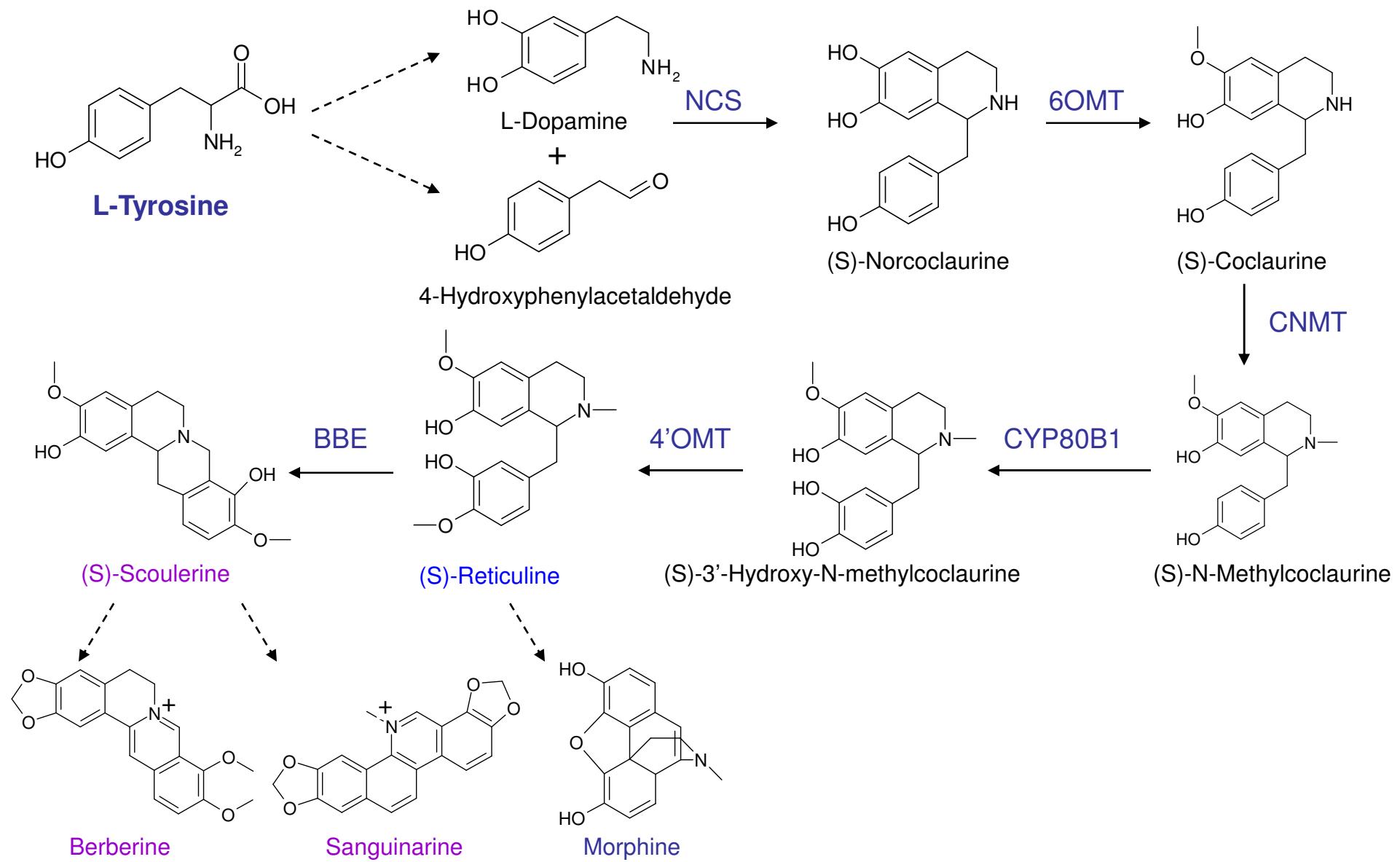


## Benzylisoquinoline alkaloid microbial synthesis



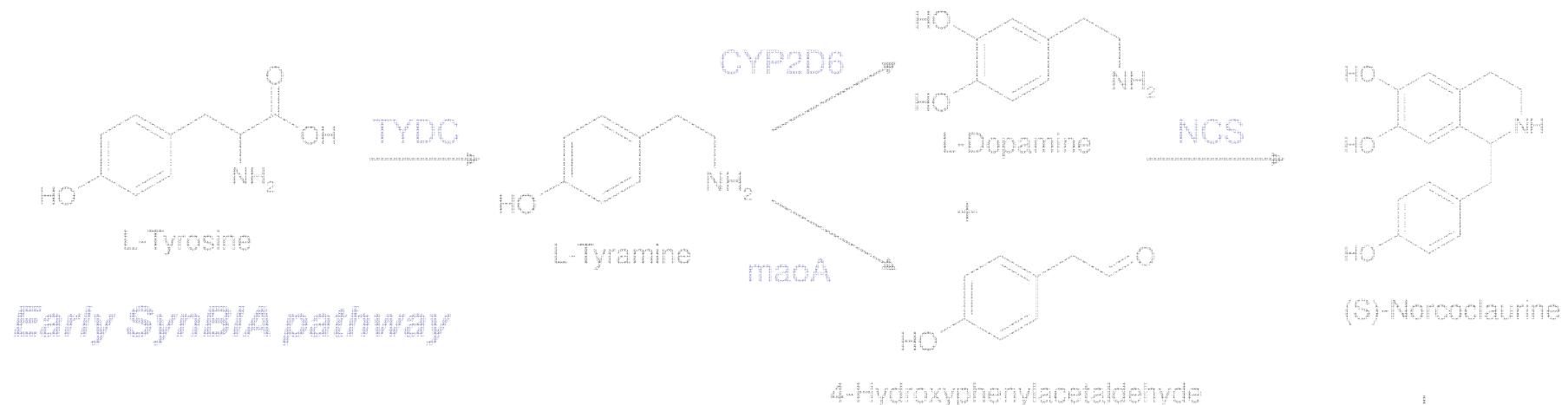
<http://www.nature.com/news/2004/040816/images/yeast.jpg>  
<http://www.westwindphotos.ca/images/101%20Opium%20Poppy.jpg>

# Native BIA pathway

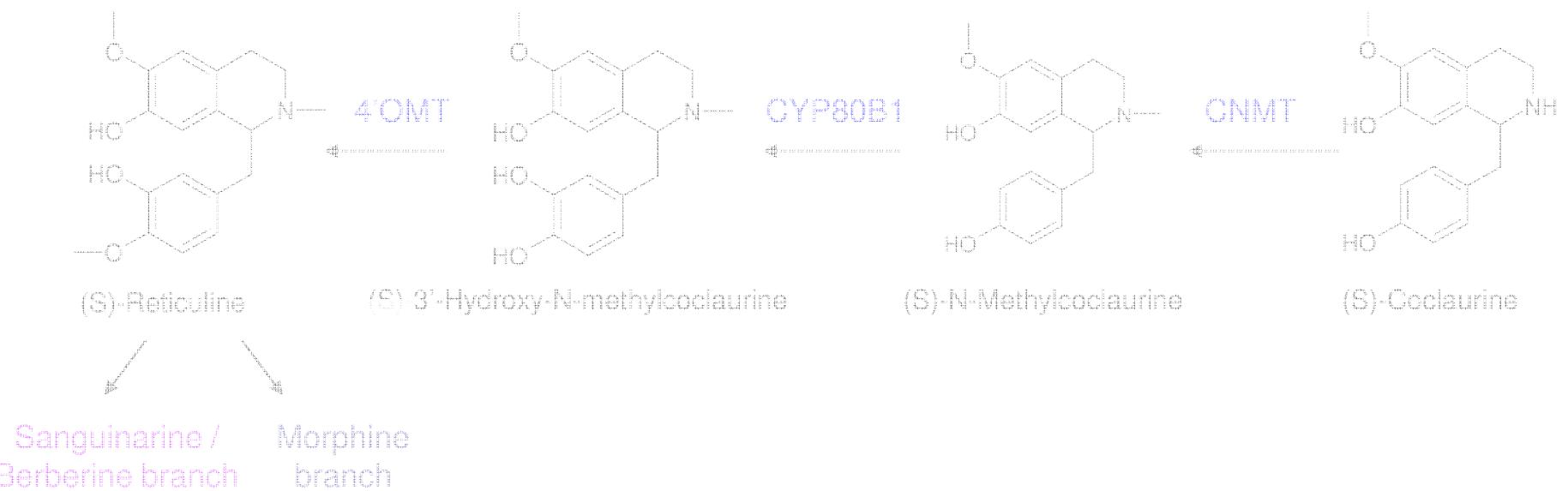


Facchini PJ. 2001. *Annu Rev Plant Physiol Plant Mol Biol*. 52: 29-66

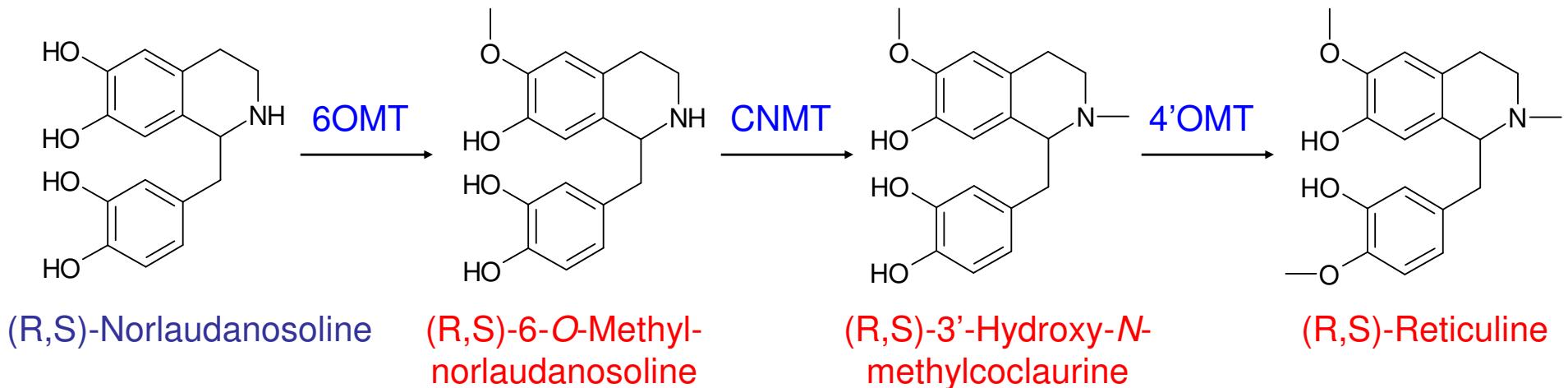
# Synthetic BIA pathway



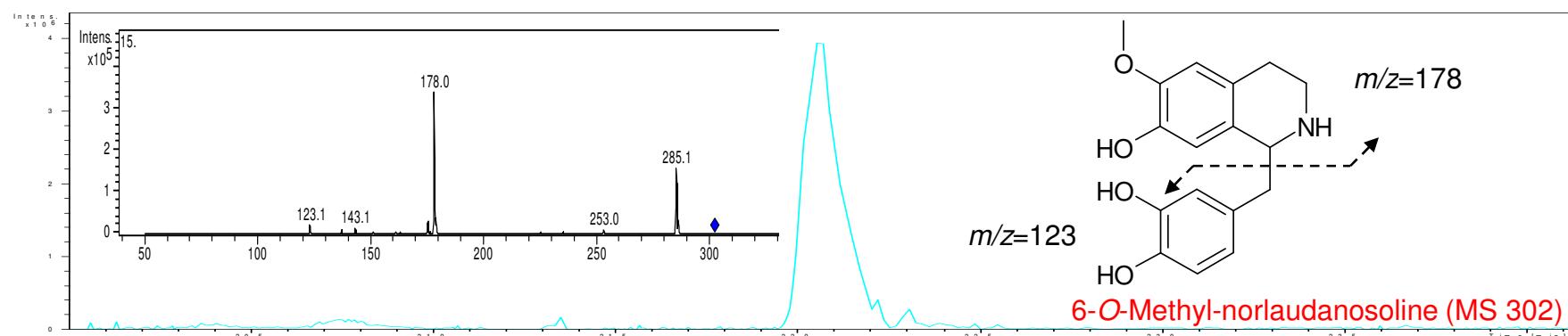
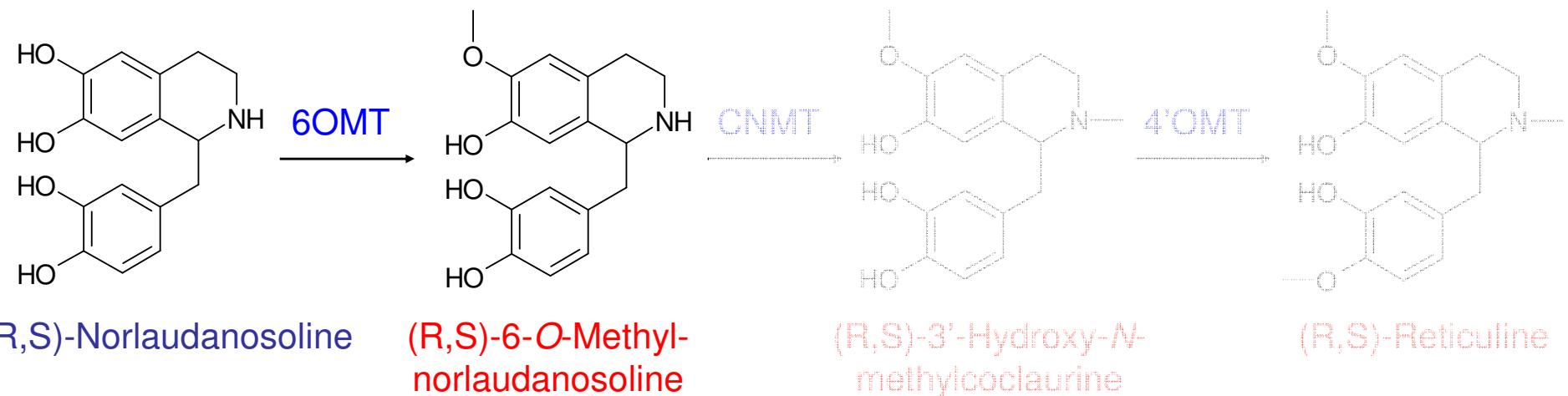
## Late SynBIA pathway



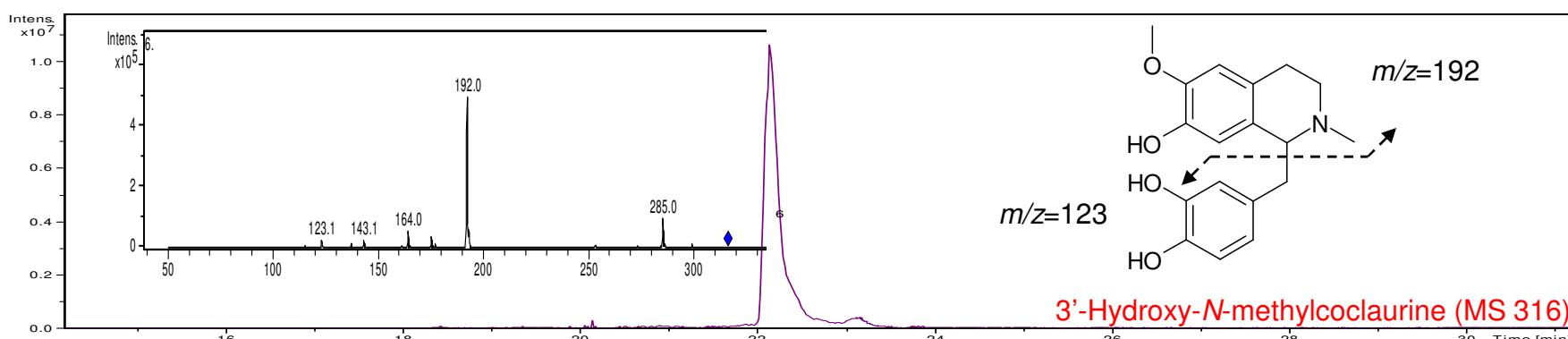
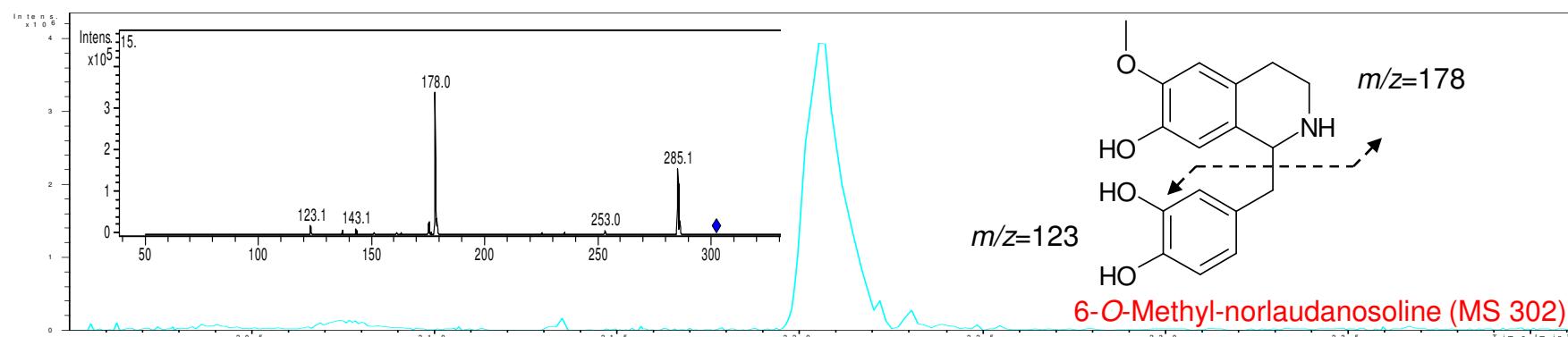
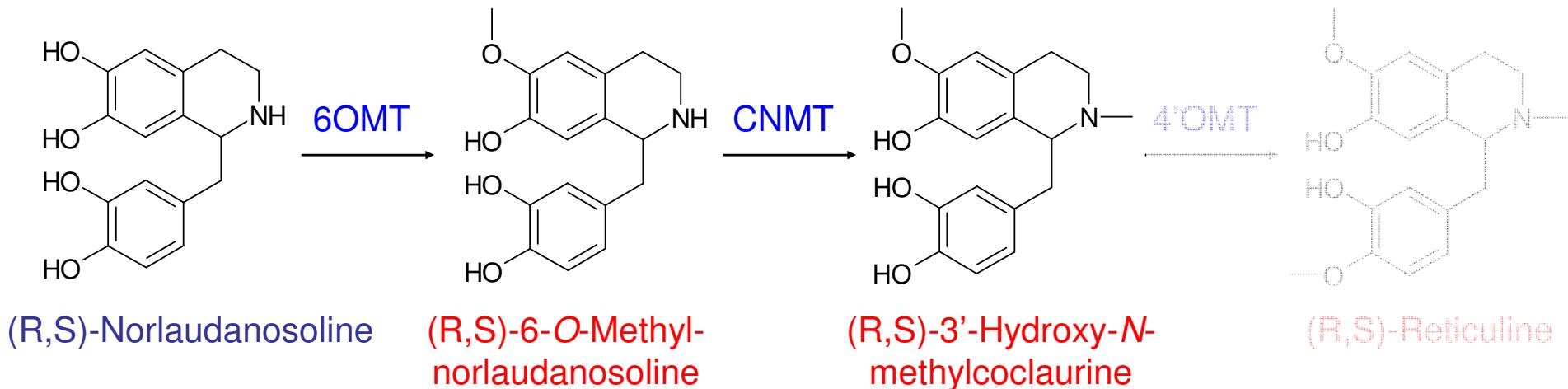
# Late Synthetic BIA pathway



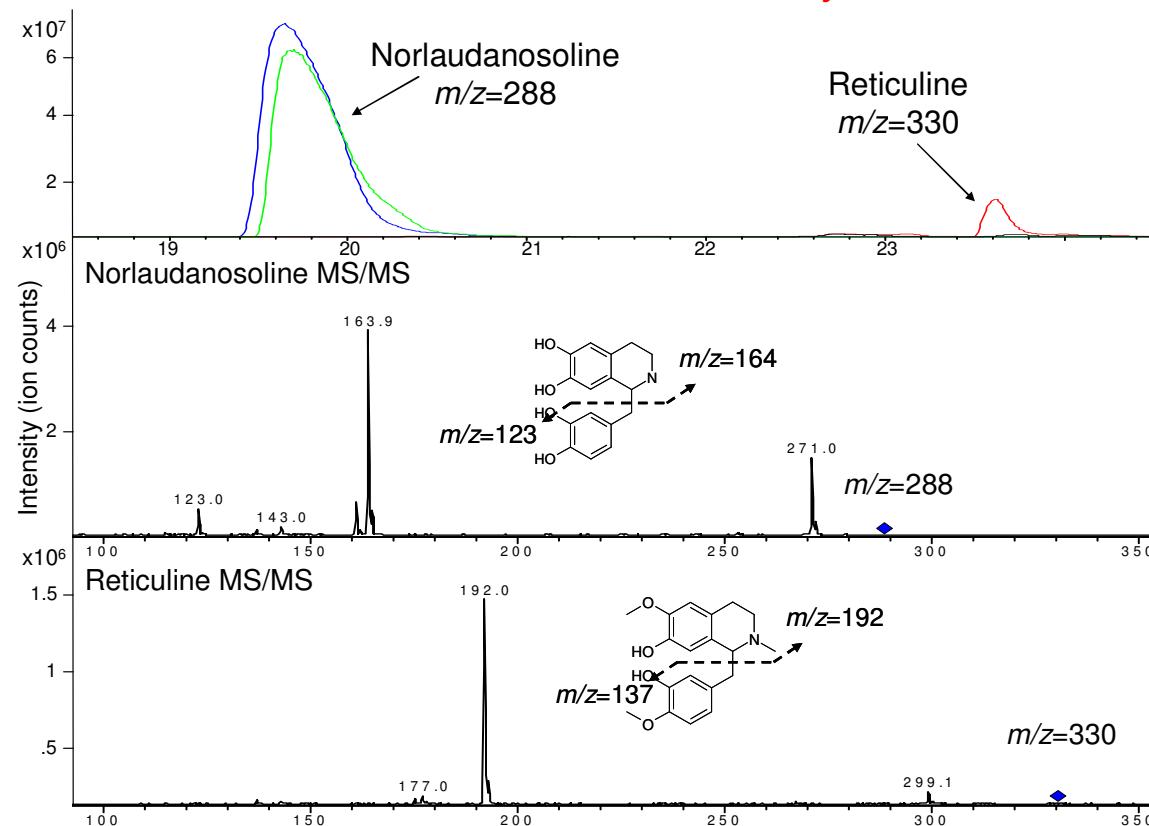
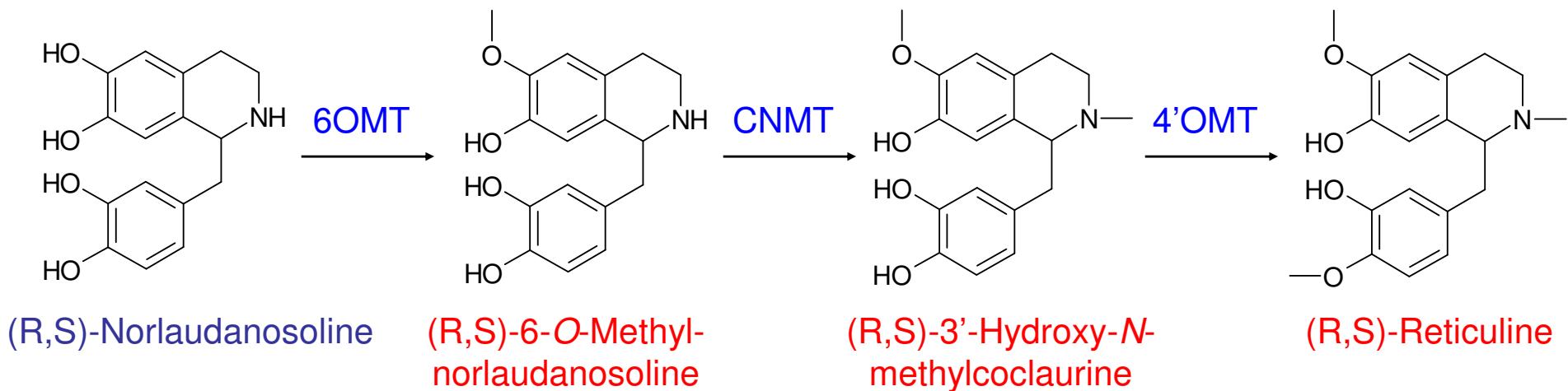
# Production of 6-O-Methyl-norlaudanosoline



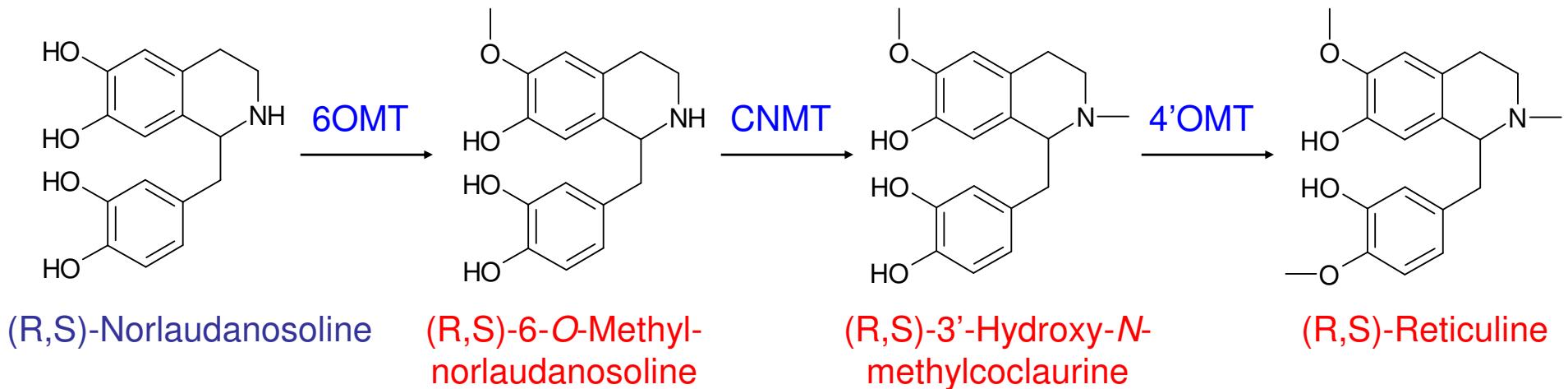
# Production of 3'-Hydroxy-N-methylcoclaurine



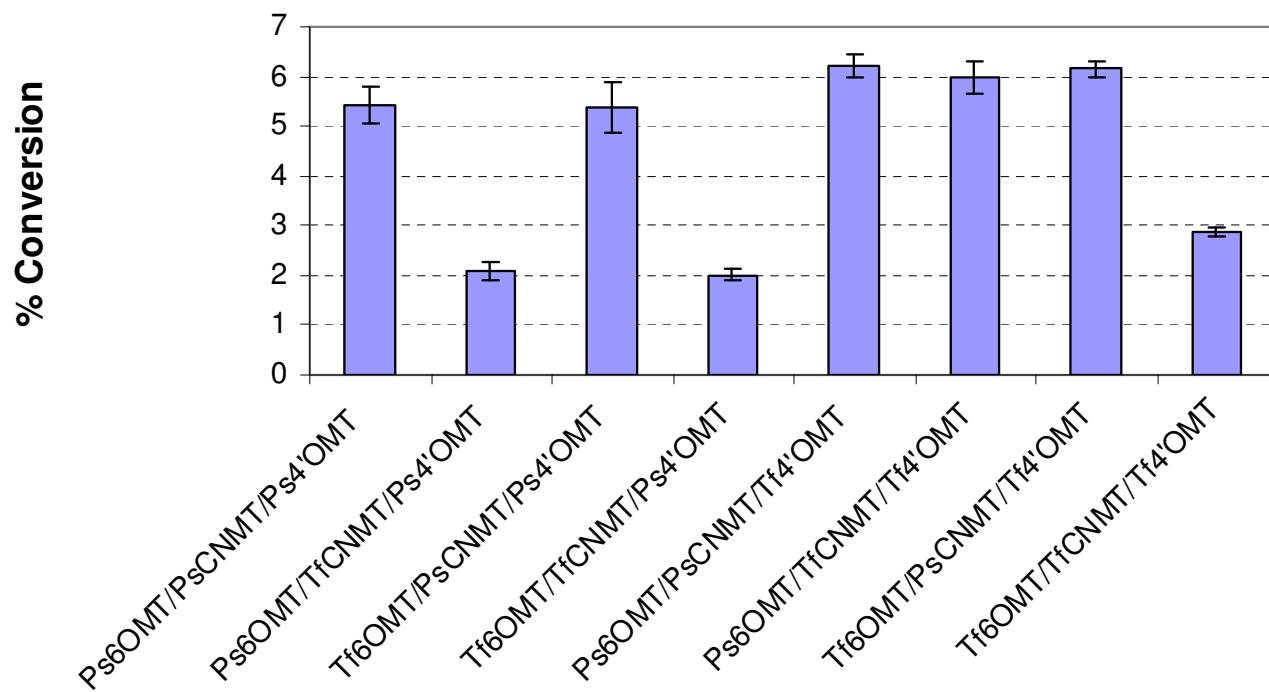
# Production of (R,S)-Reticuline



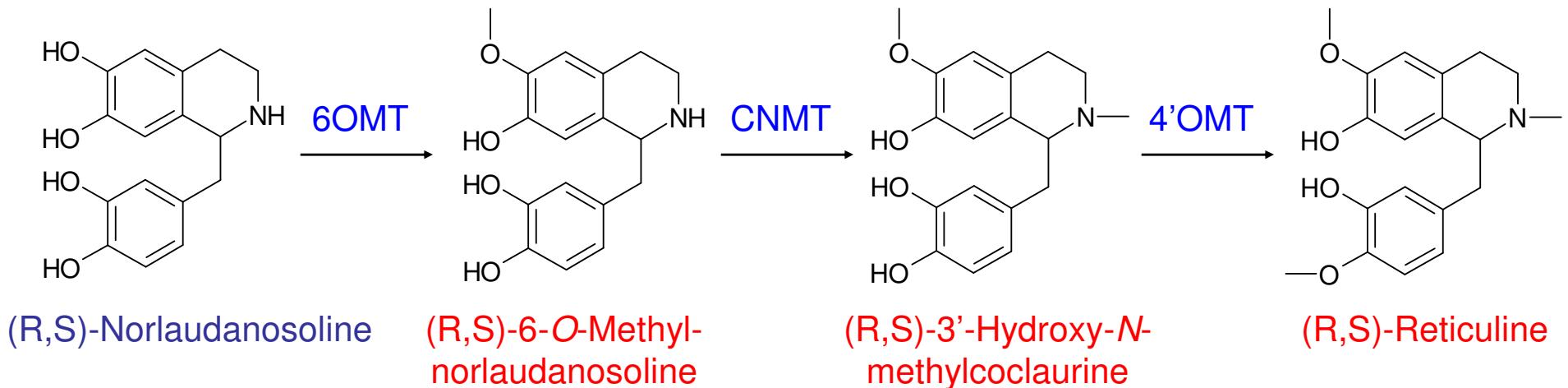
# Optimization of (R,S)-Reticuline production



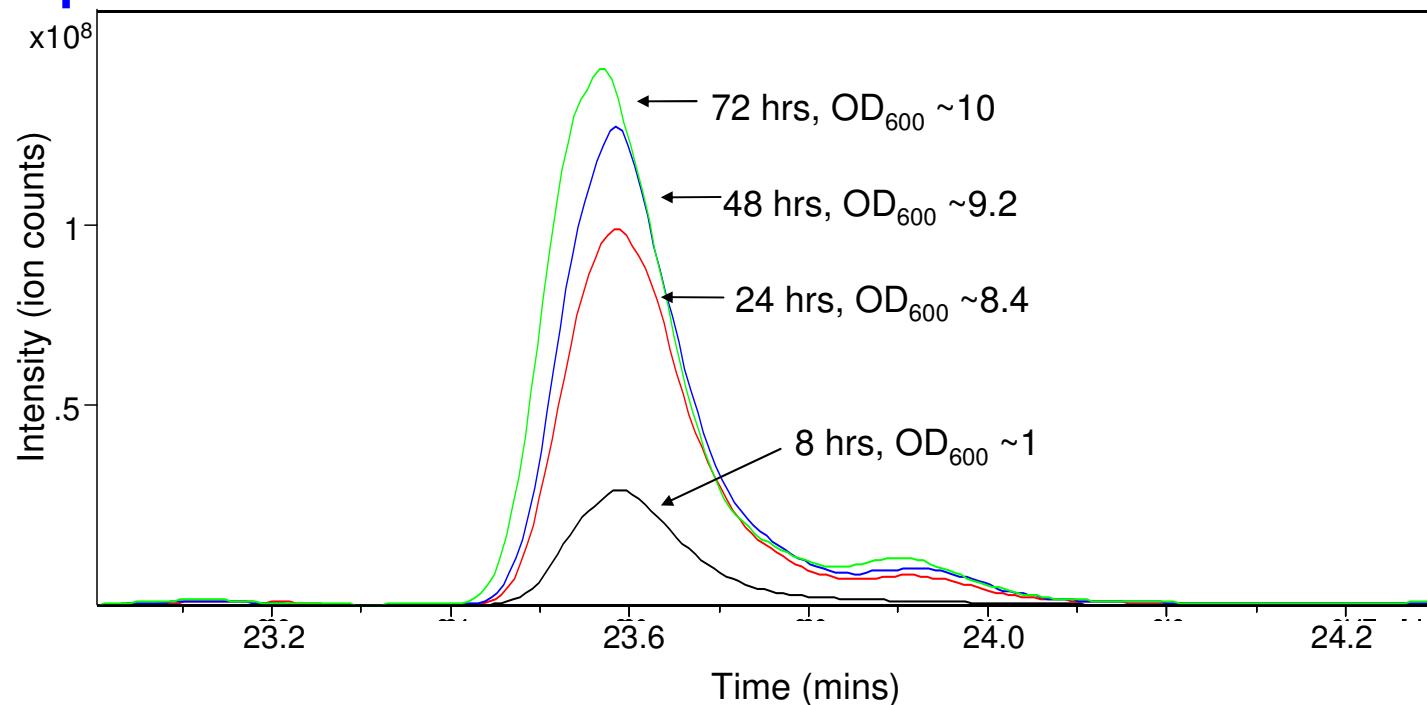
## Enzyme variant dependence:



# Optimization of (R,S)-Reticuline production

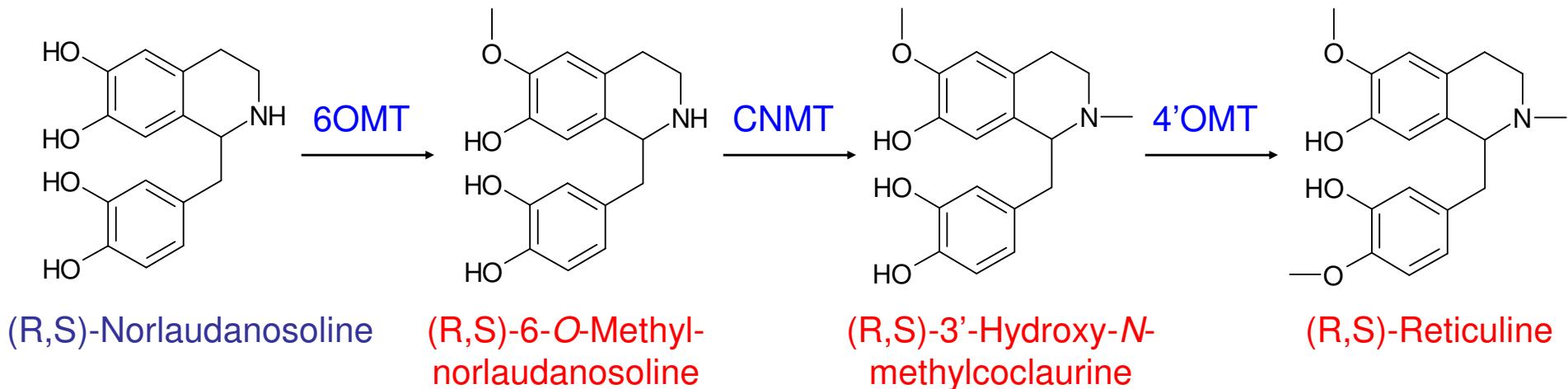


## Time dependence:

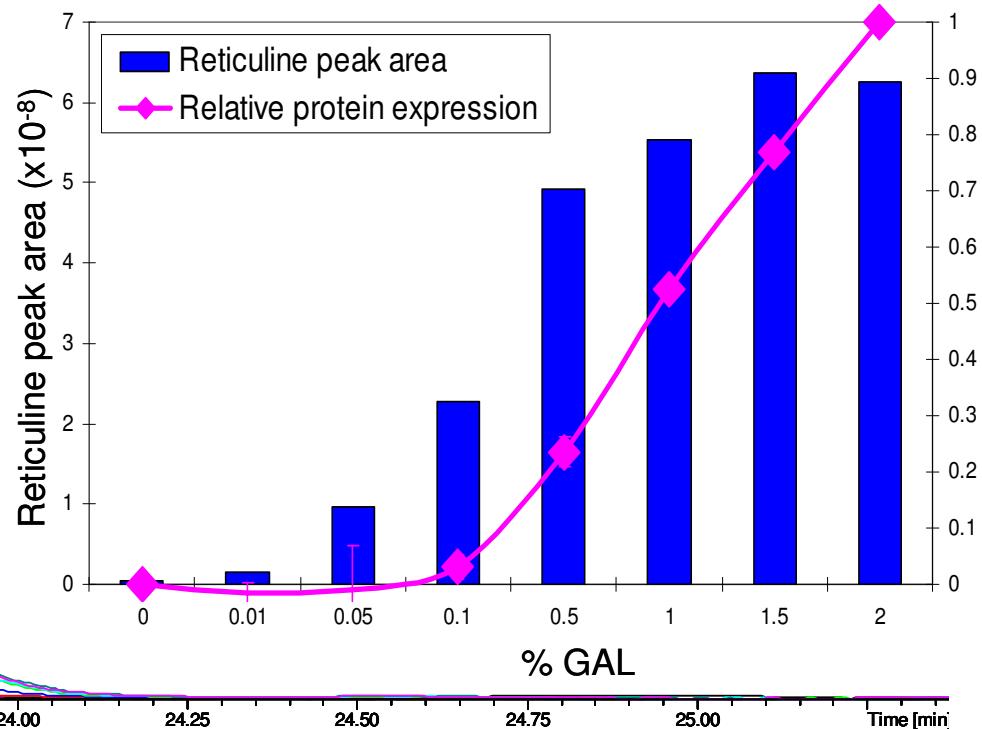
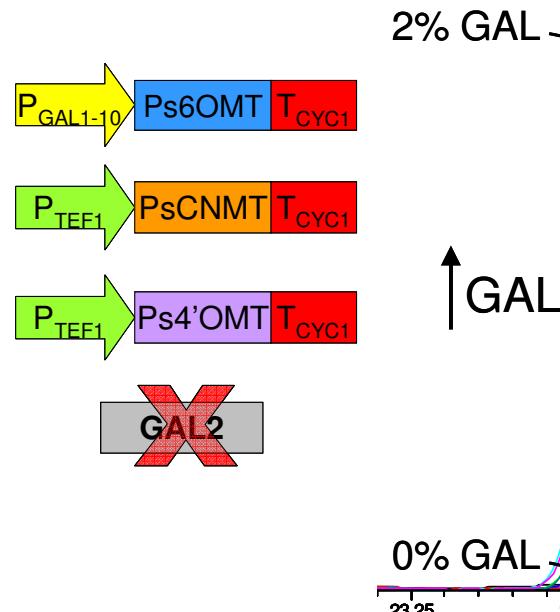


Strains continue to accumulate (R, S)-Reticuline during growth in stationary phase ( $OD_{600} \sim 10$ ).

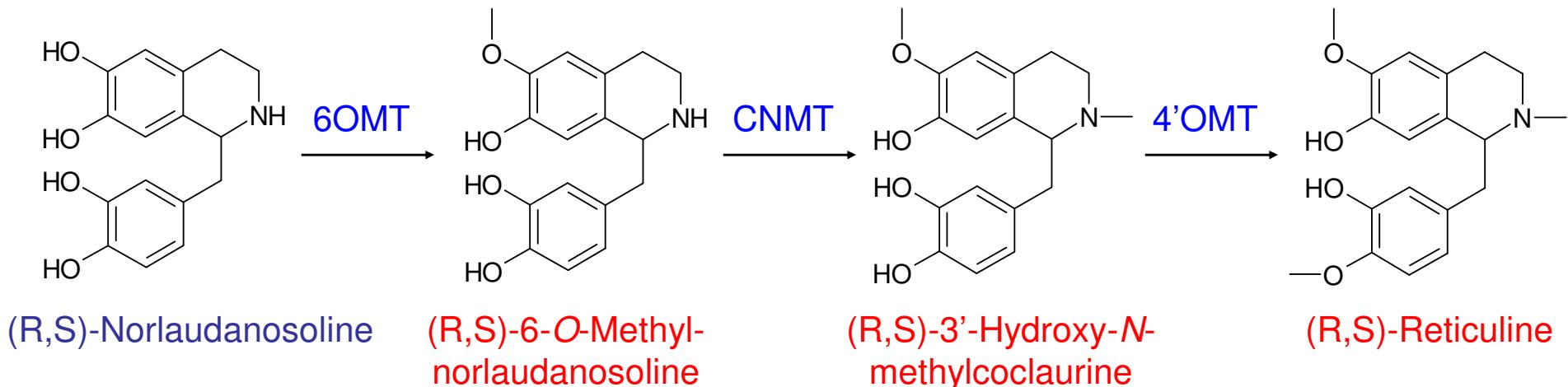
# Optimization of (R,S)-Reticuline production



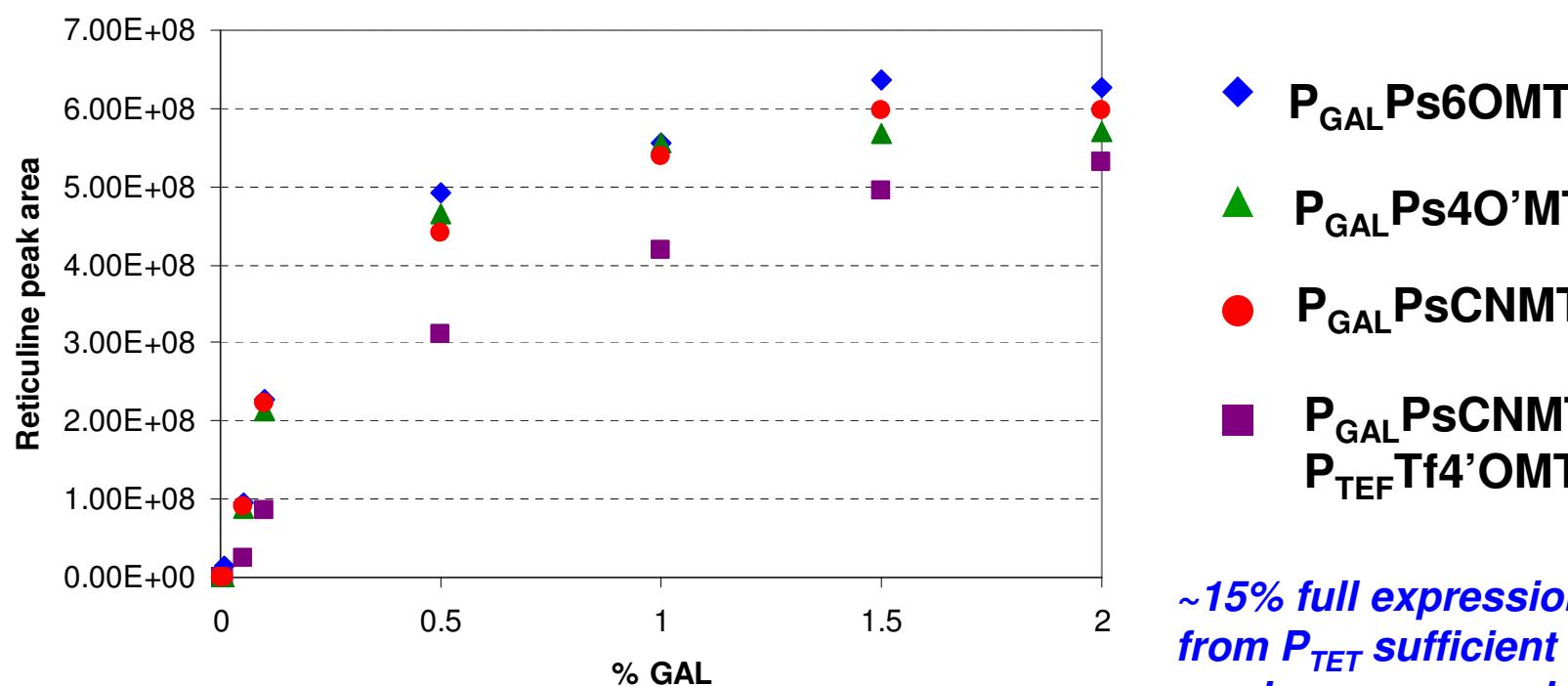
## Enzyme level dependence:



# Optimization of (R,S)-Reticuline production

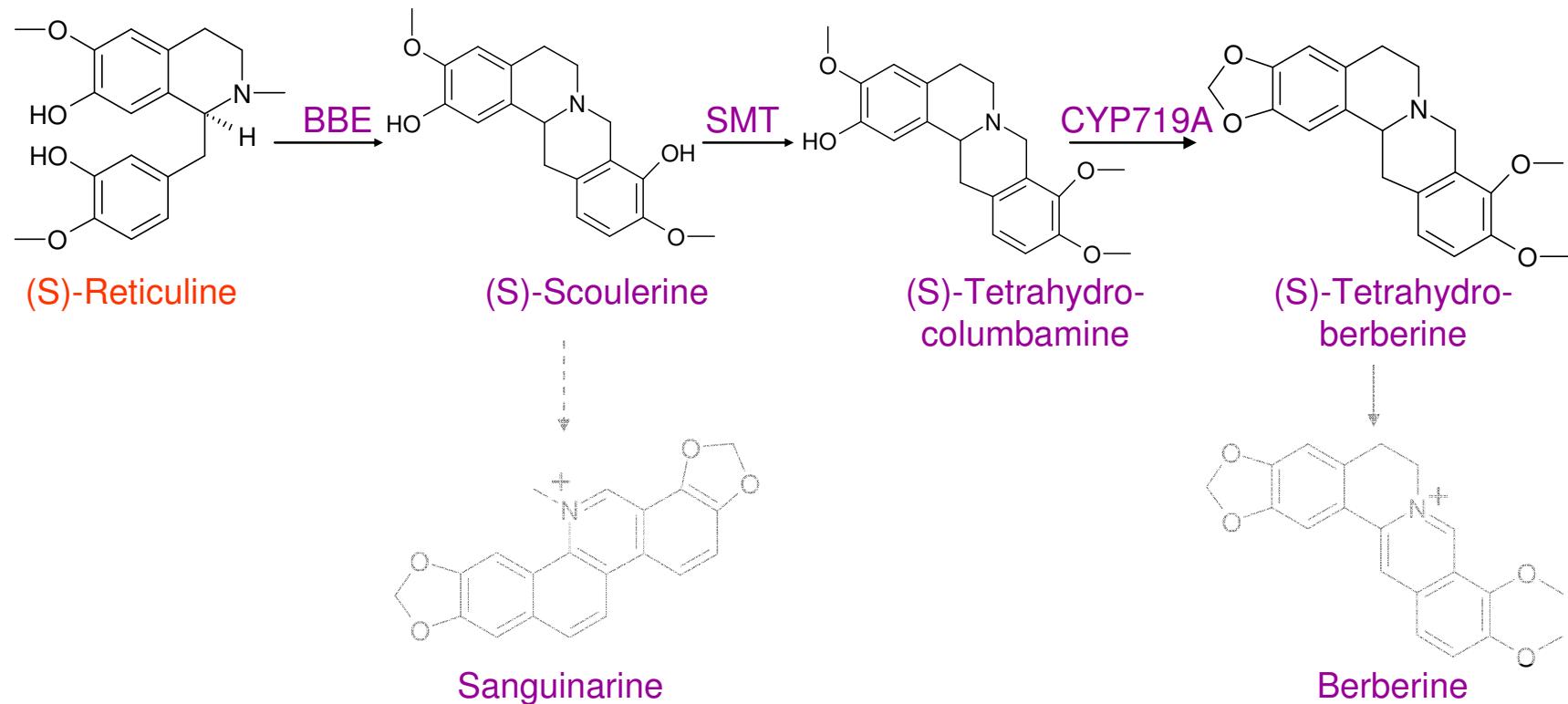


## Enzyme level dependence:

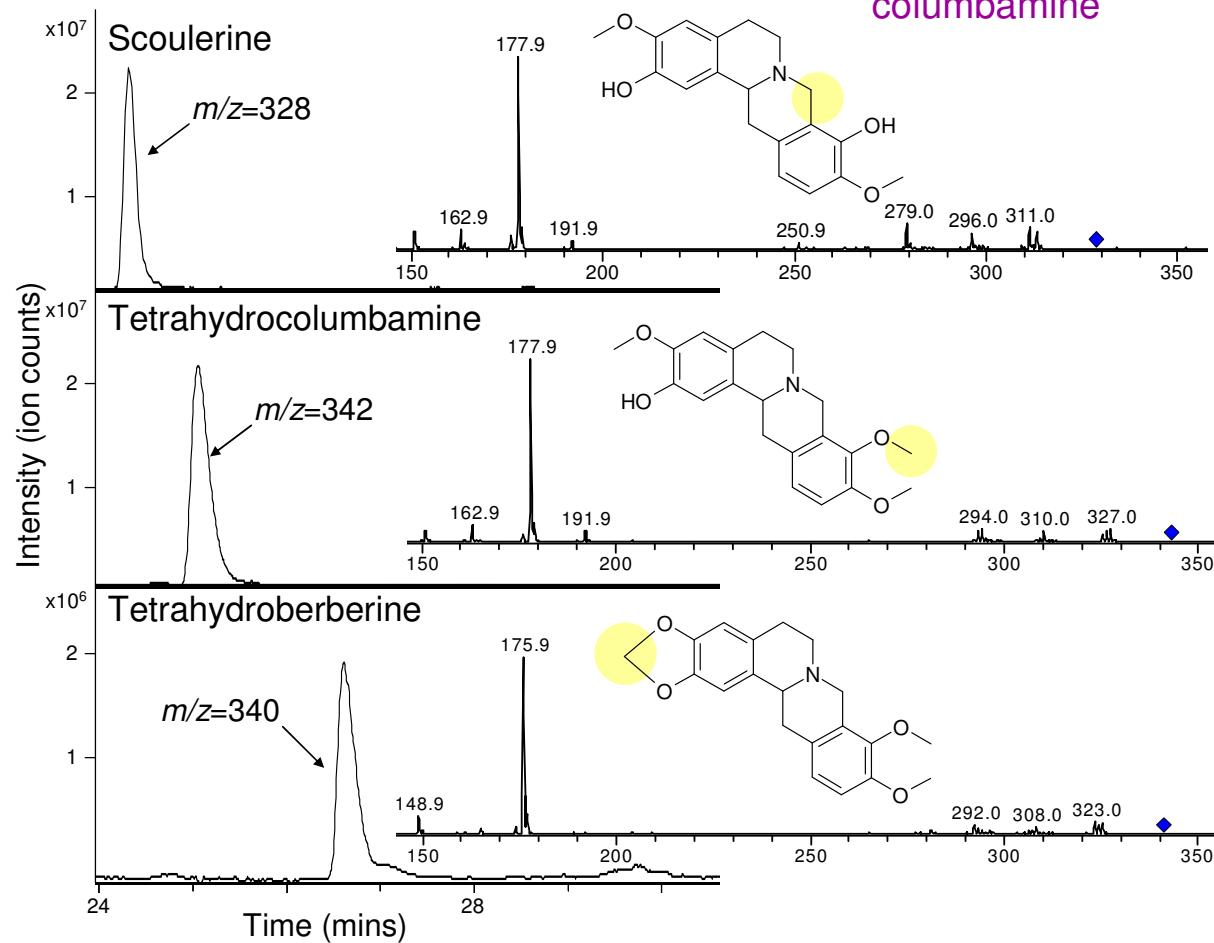
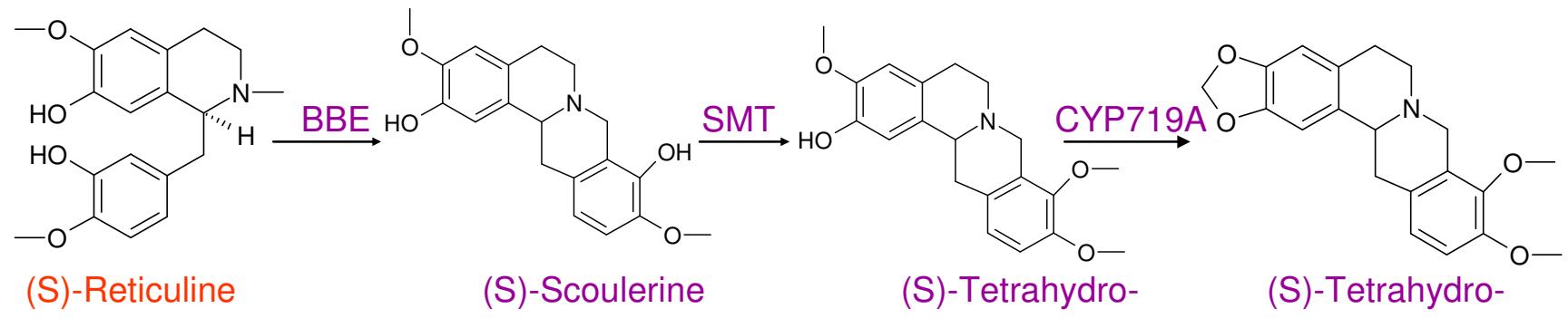


*~15% full expression levels  
from  $P_{TET}$  sufficient for  
maximum conversion*

# BIA synthesis beyond reticuline – berberine branch



# BIA synthesis beyond reticuline – berberine branch

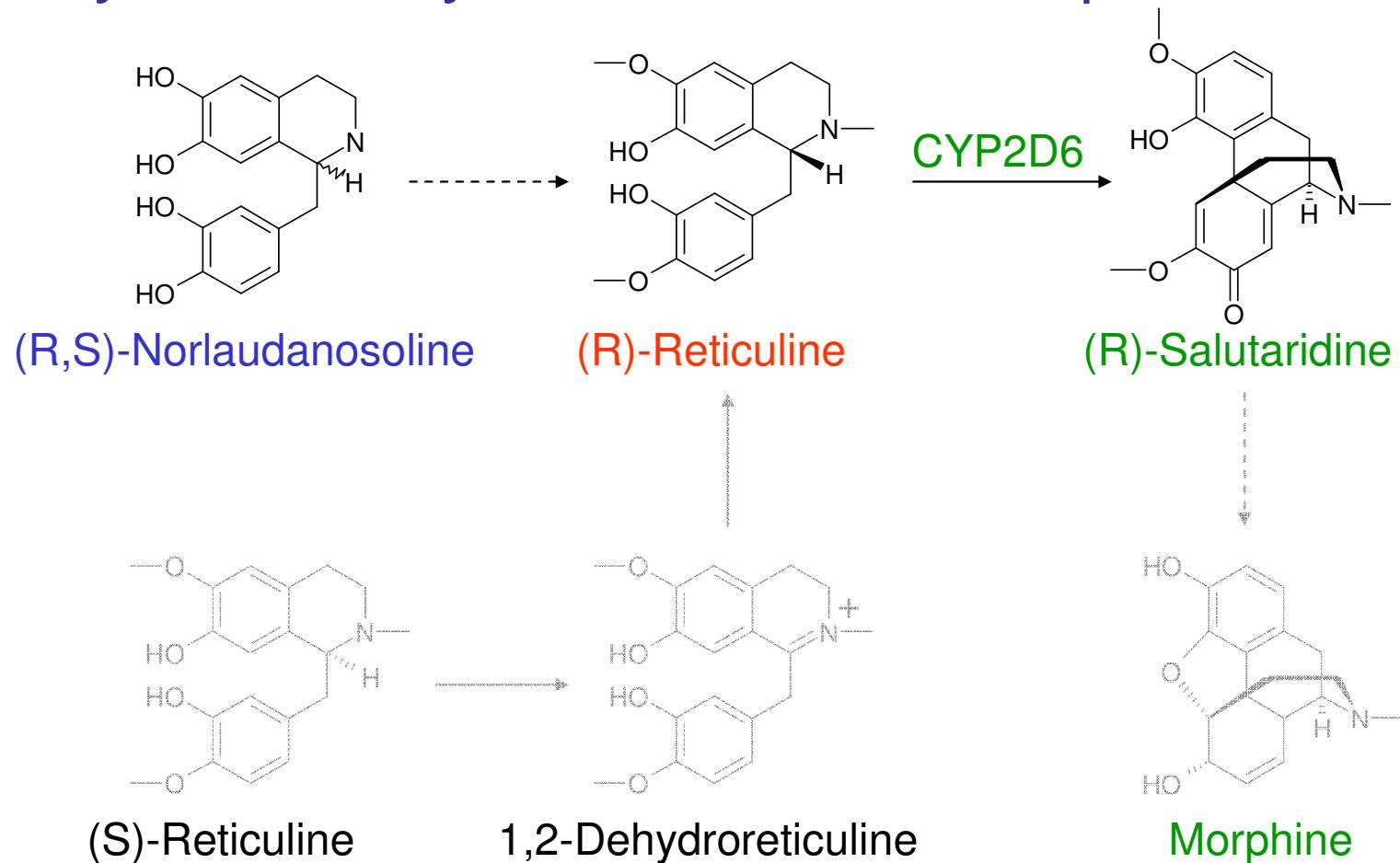


PsBBE

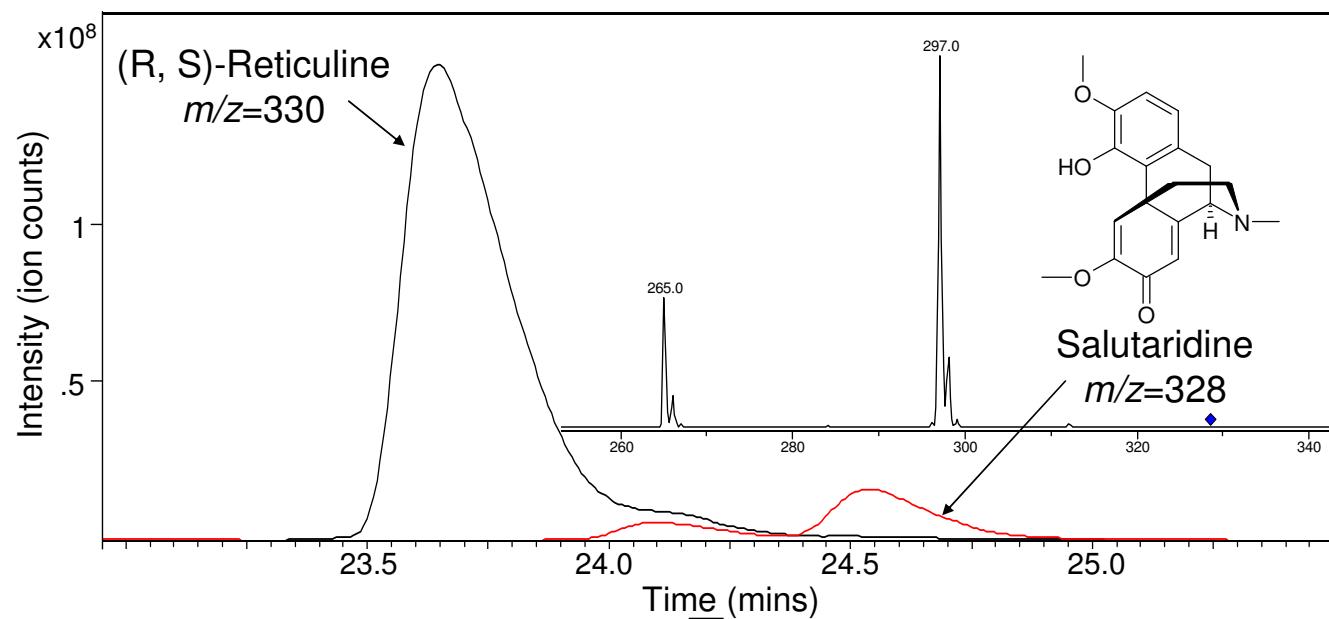
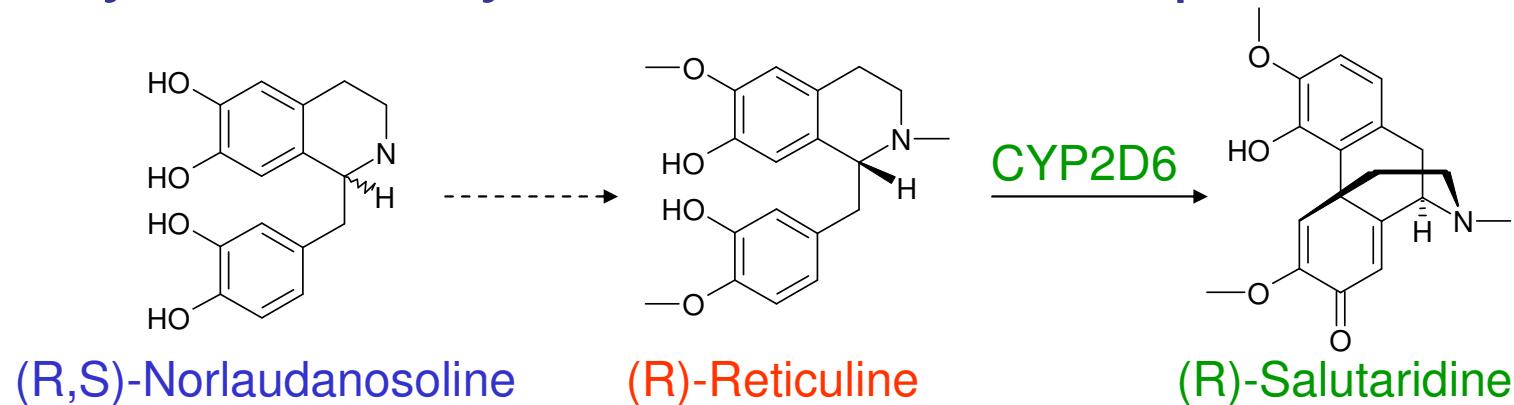
TfSMT

TfCYP719A  
AtATR1

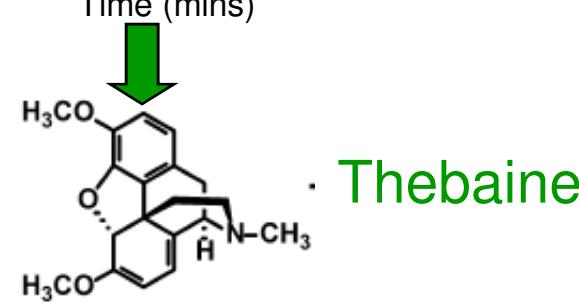
# BIA synthesis beyond reticuline – morphine branch



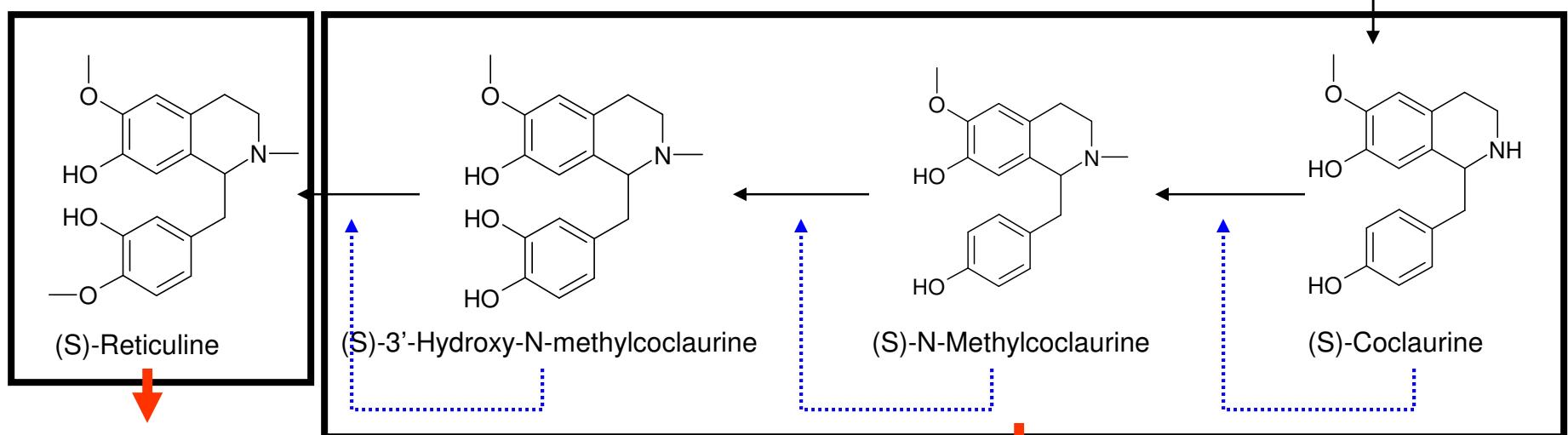
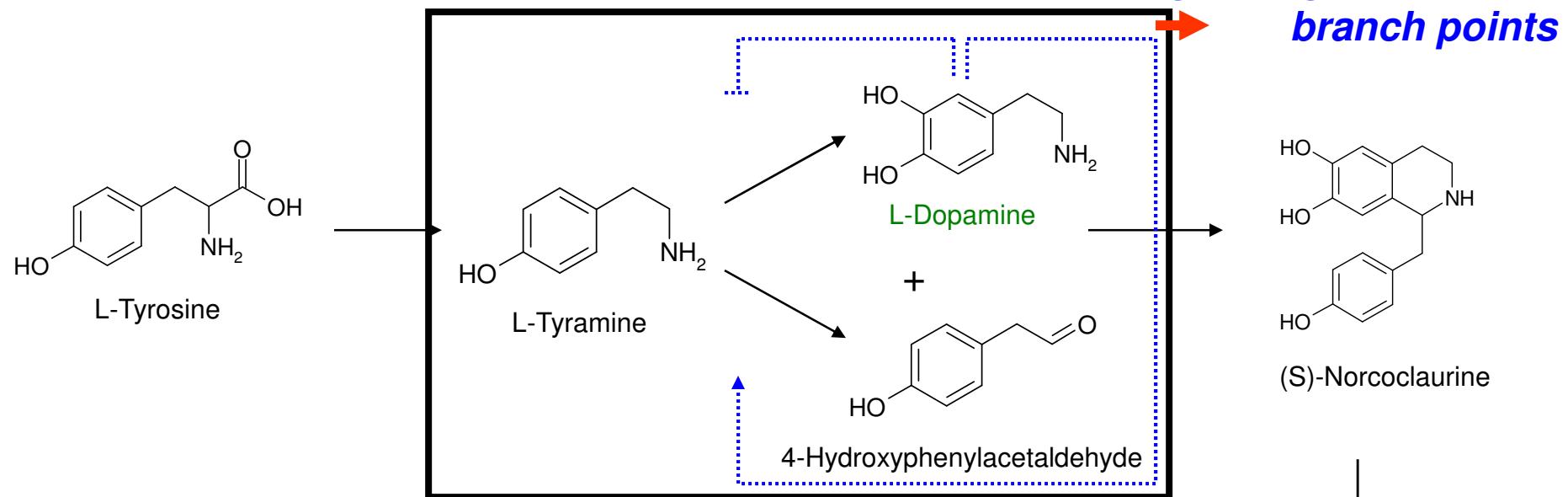
# BIA synthesis beyond reticuline – morphine branch



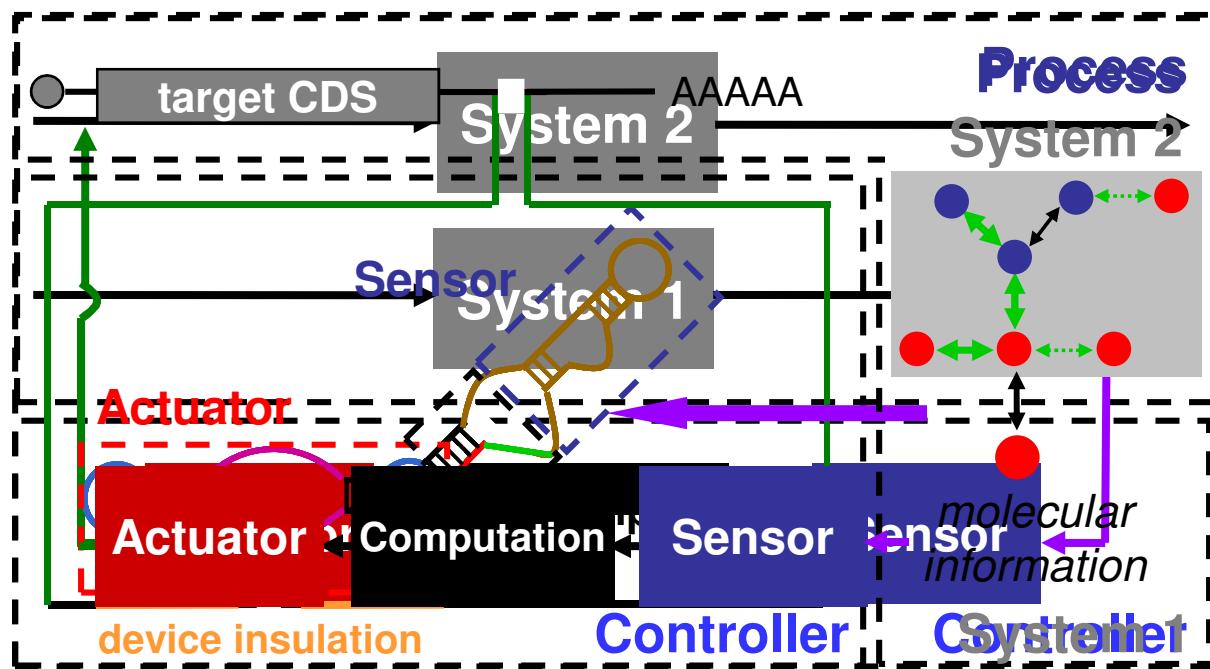
HsCYP2D6



# Tools for optimizing BIA production

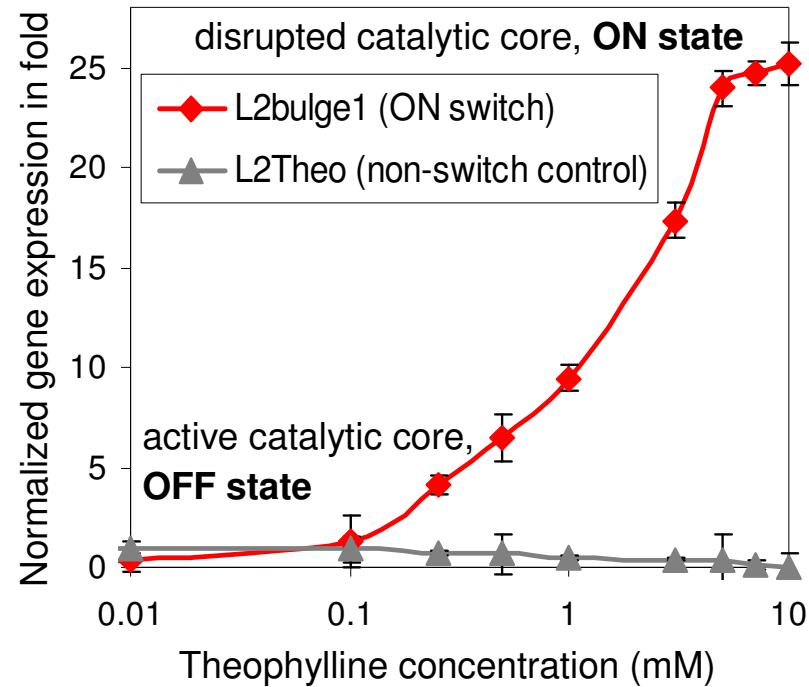
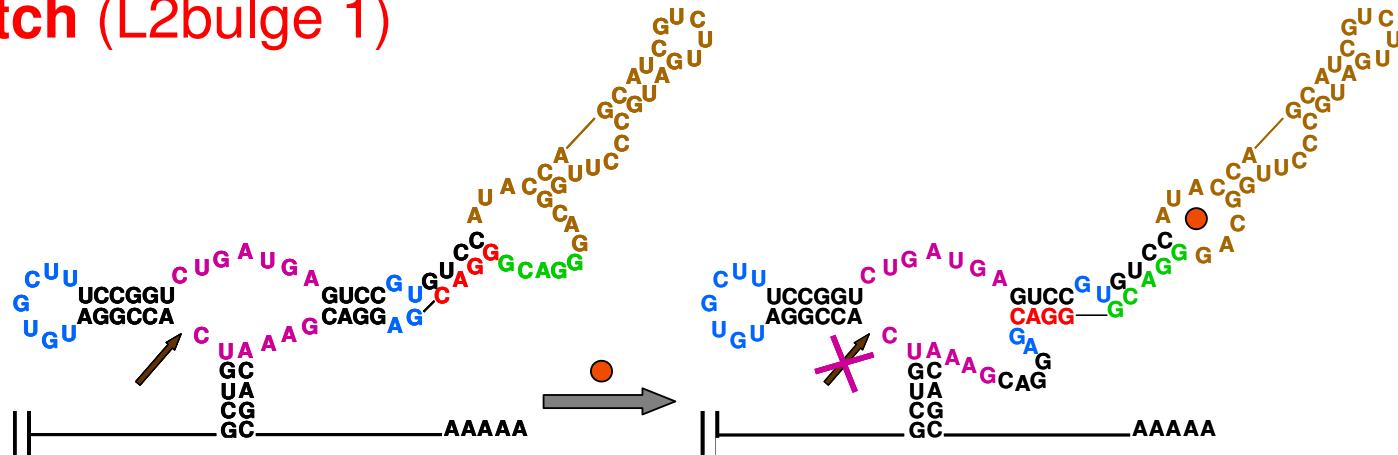


# General biological control system



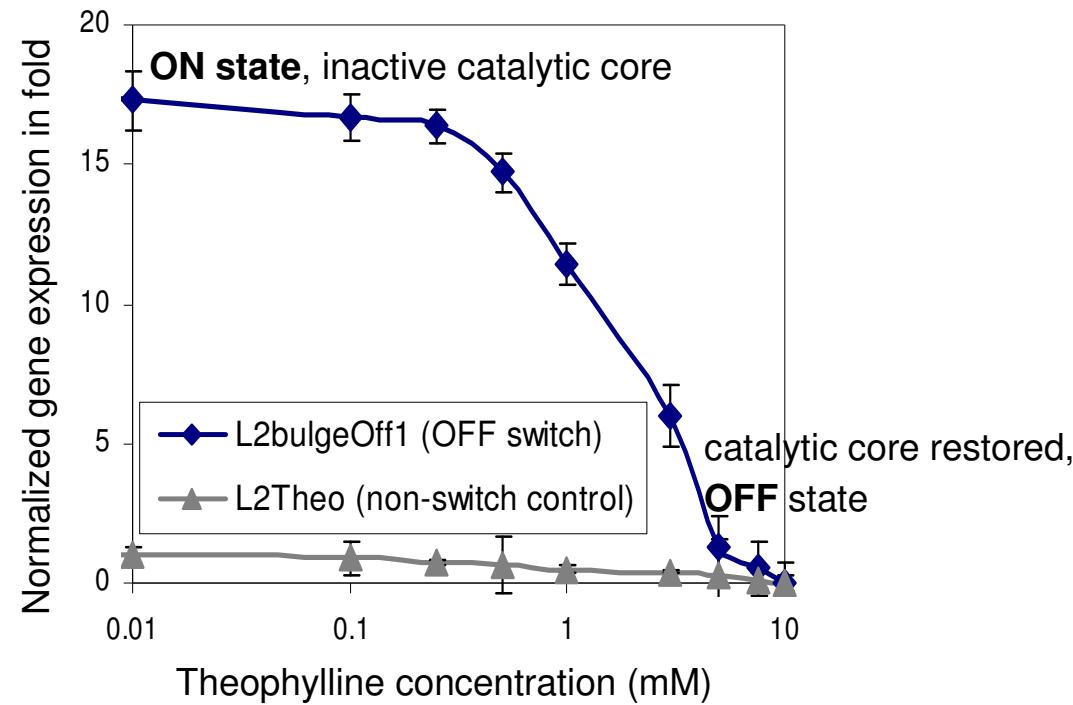
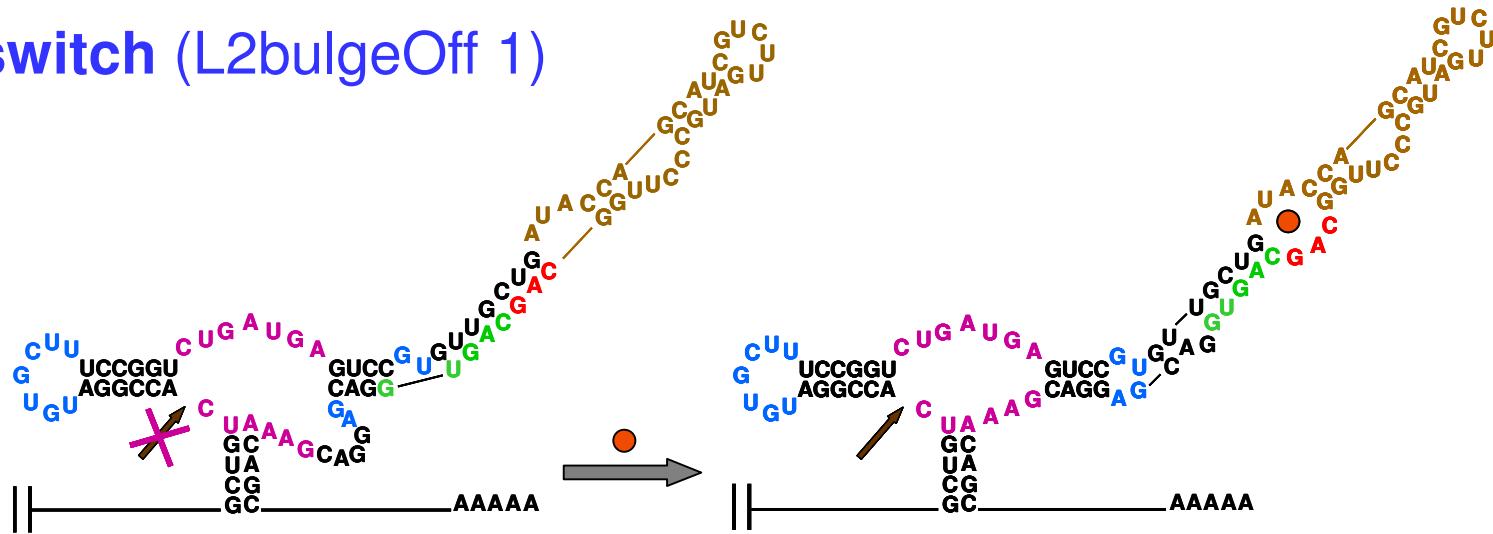
# A ribozyme switch platform for up-regulating expression

## ON switch (L2bulge 1)

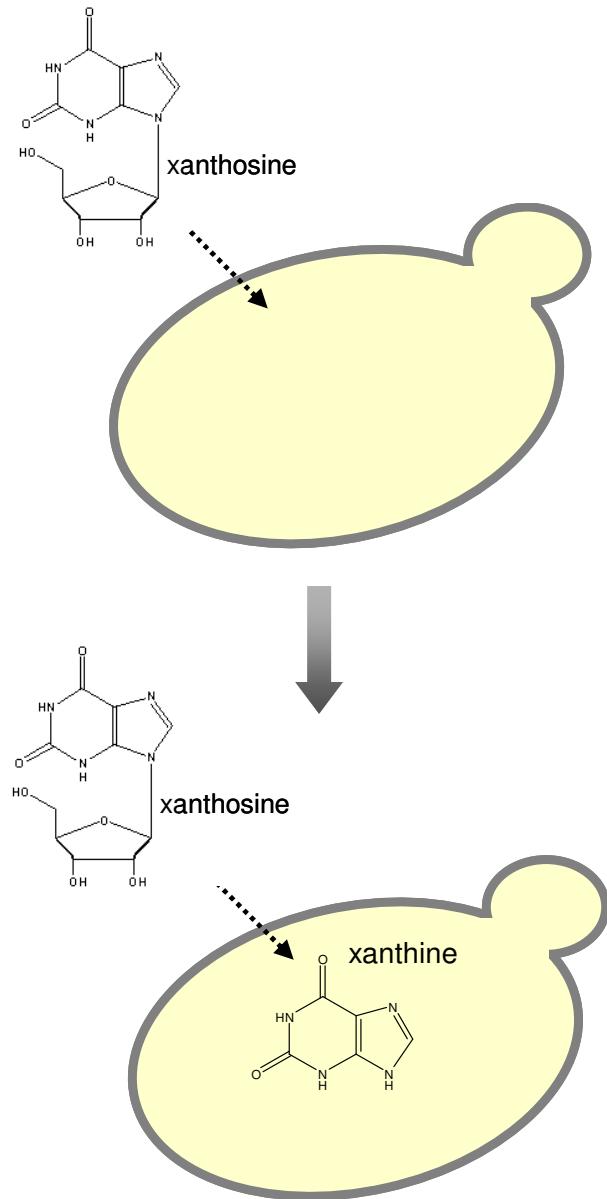


# A ribozyme switch platform for down-regulating expression

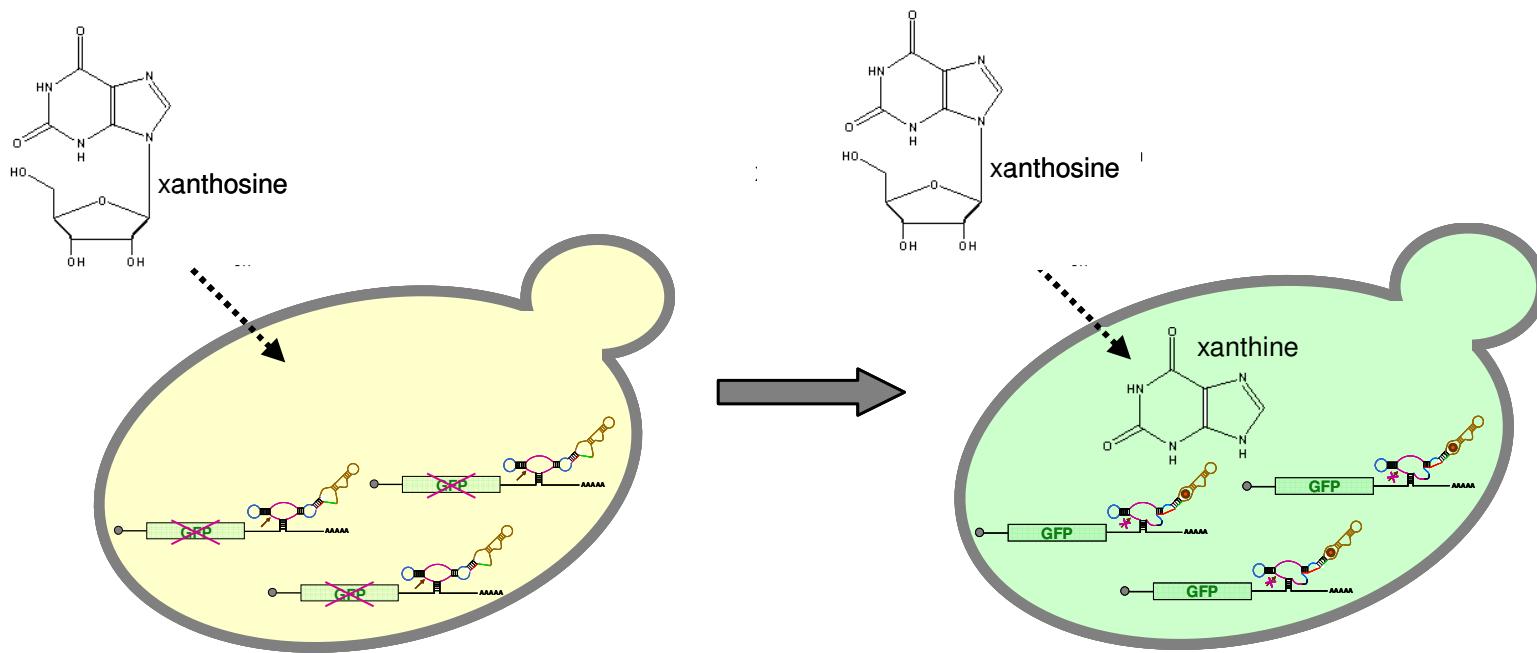
## OFF switch (L2bulgeOff 1)

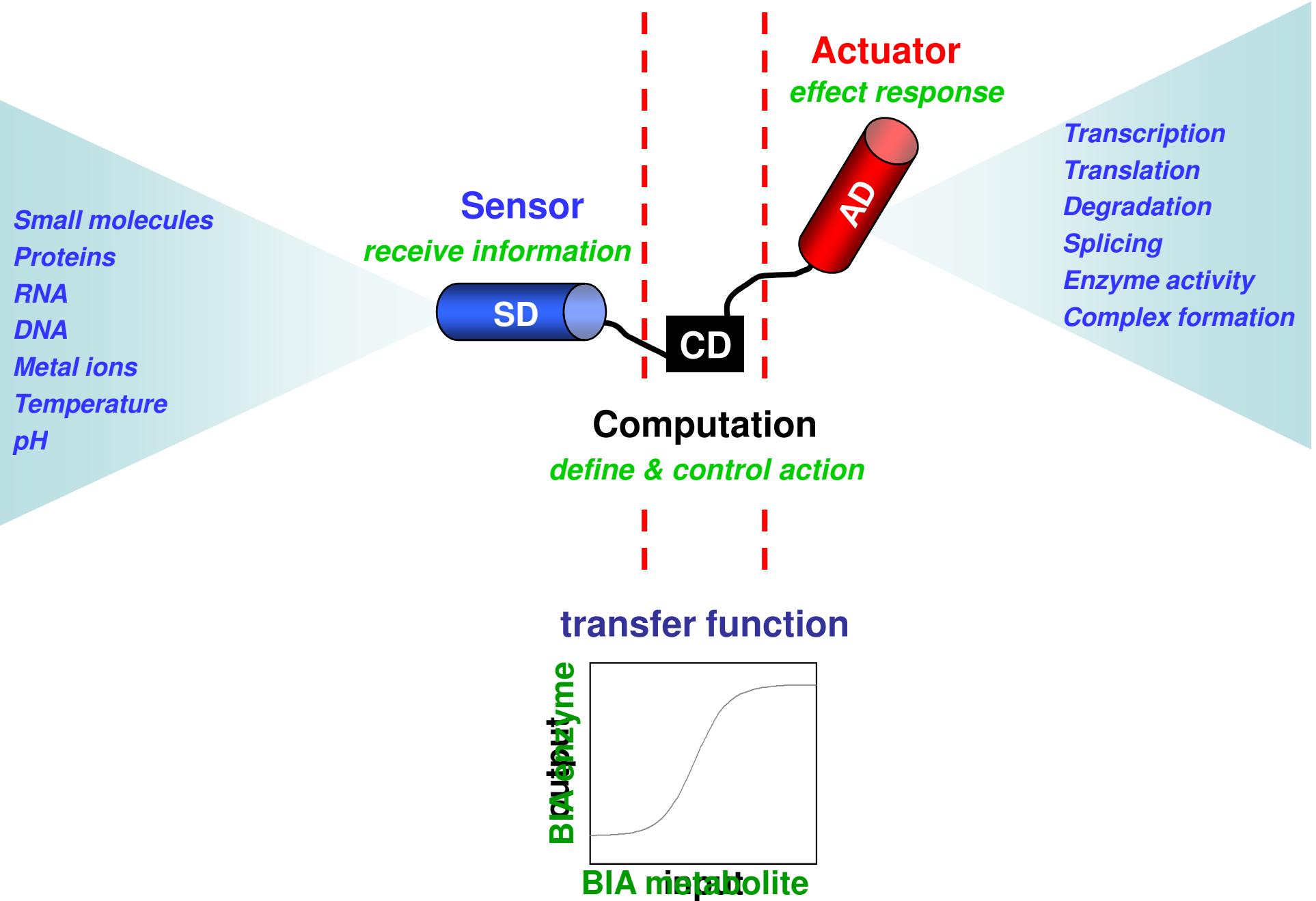


# Integrating RNA devices as noninvasive sensors of metabolite concentration



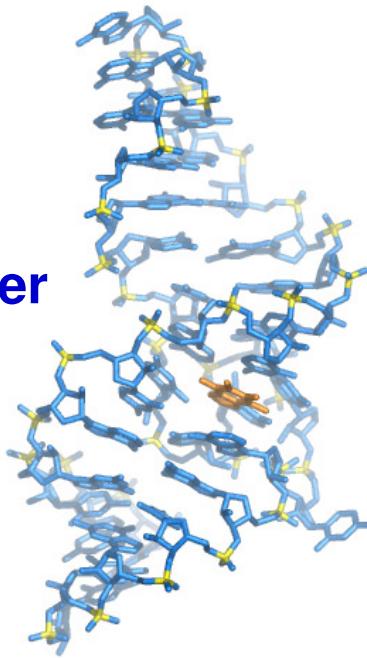
# Integrating RNA devices as noninvasive sensors of metabolite concentration



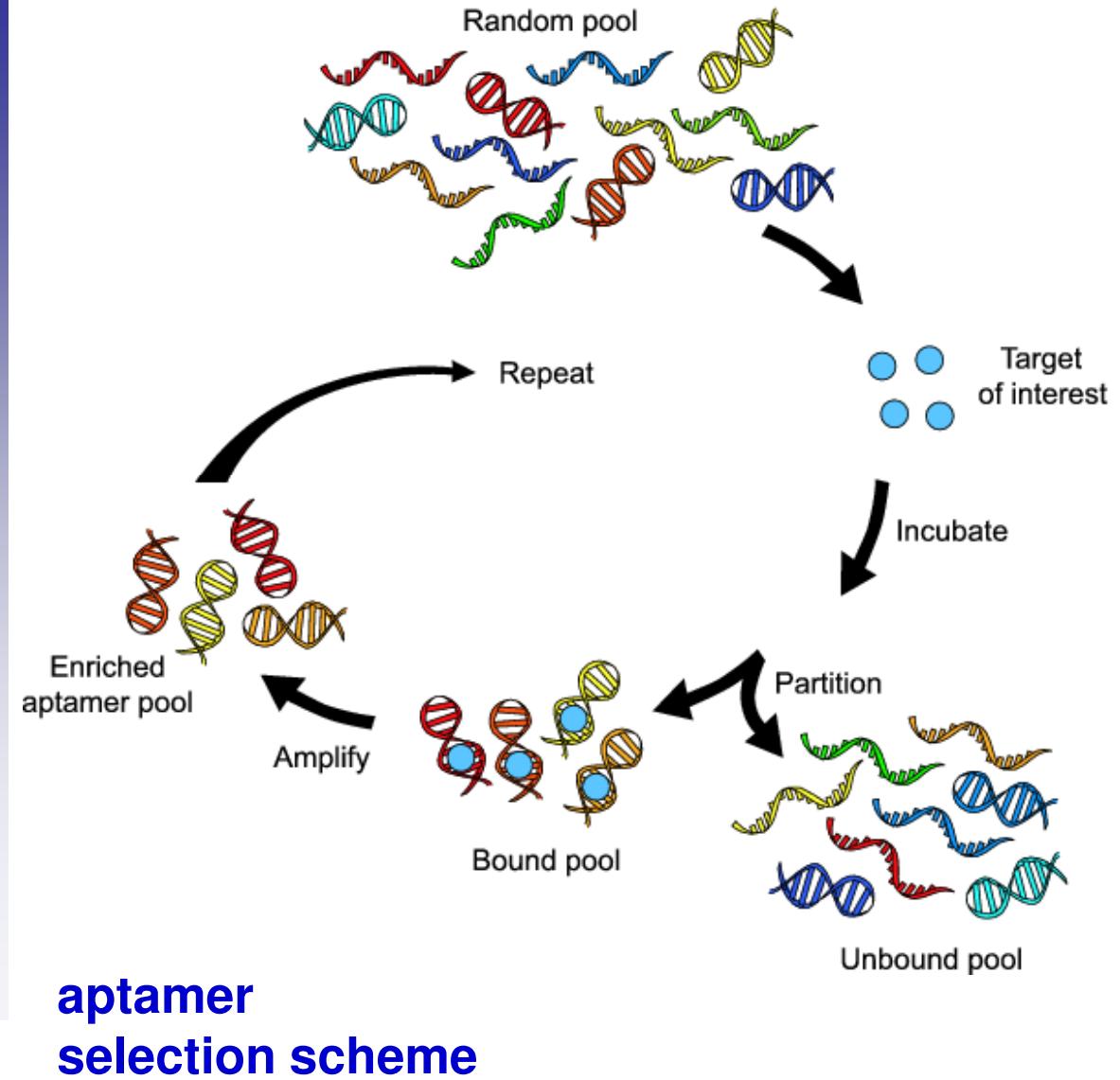


# Scalability challenge: libraries of nucleic acid sensors

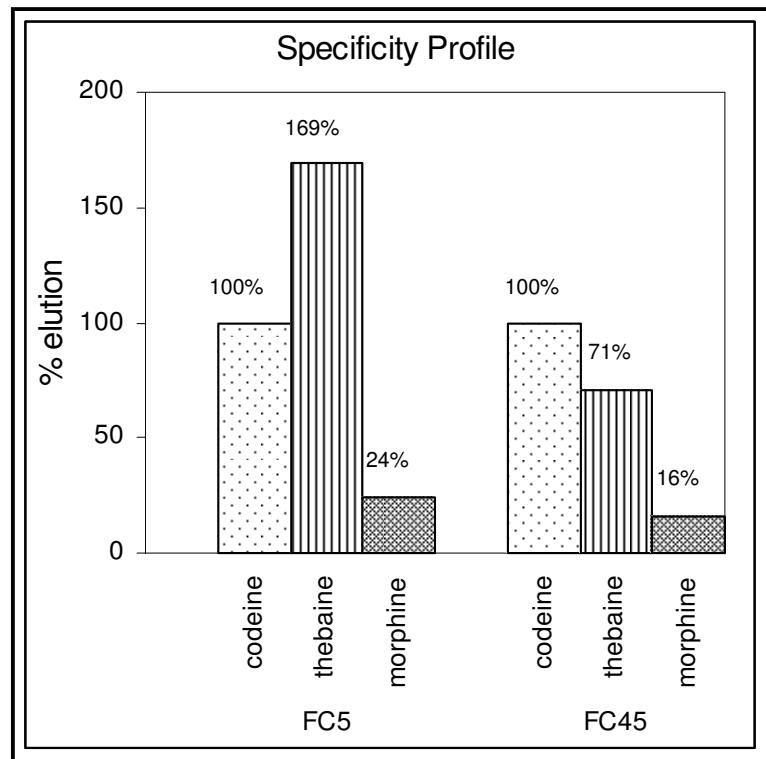
aptamer



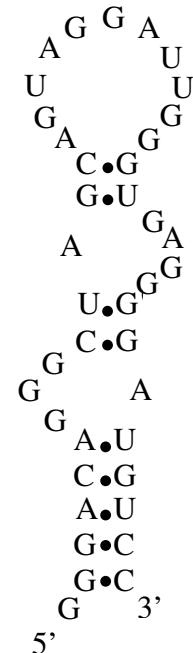
- bind wide range of ligands
- high specificity and affinity
- generated through *in vitro* selection process



# Specificities of BIA-binding aptamers

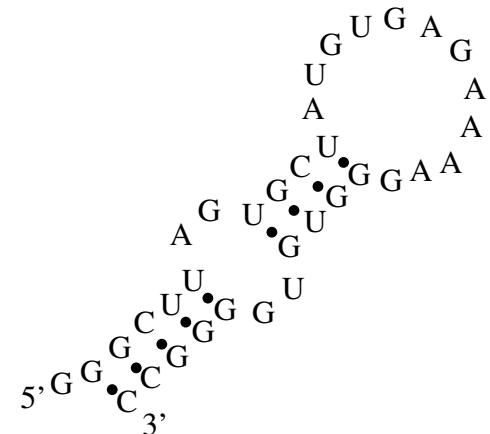


**FC5**

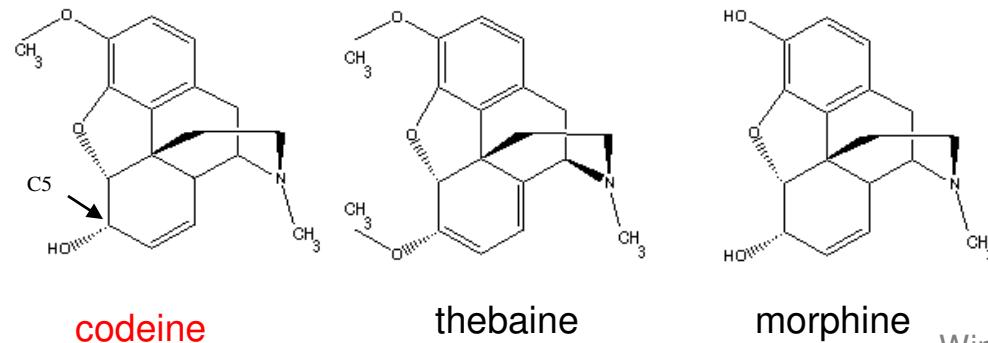


$$K_d (\text{FC5L}) = 4.55 \pm 0.14 \mu\text{M}$$

**FC45**



$$K_d (\text{FC45L}) = 2.59 \pm 0.09 \mu\text{M}$$



***High-throughput SPR-based characterization strategy enables rapid screening for mini-aptamer sequences and structural analysis***

Win MN, Klein JS, Smolke CD. 2006. *Nuc Acids Res.* 34: 5670-82.

# Integrating synthetic metabolic networks and RNA-based control systems

- Metabolic pathway engineering requires a host of tools for optimizing flux and product accumulation
- User-programmed feedback control systems are useful for dynamically controlling flux through pathways
- Developing new genetically encoded tools for receiving, processing, and transmitting molecular information
- Response properties can be programmed to fit the performance specifications of a given application
- These technologies will advance the engineering of more robust cellular systems

# Acknowledgements

## The Smolke Lab

### Postdoctoral Researchers

Kevin Hoff

### Graduate Researchers

Andrew Babiskin

Chase Beisel

### **Arwen Brown**

Yvonne Chen

Stephanie Culler

Leo d'Espaux

Katie Galloway

### **Kristy Hawkins**

### **Joe Liang**

### **Josh Michener**

### **Michael Siddiqui**

Jay Vowles

### **Maung Nyan Win**

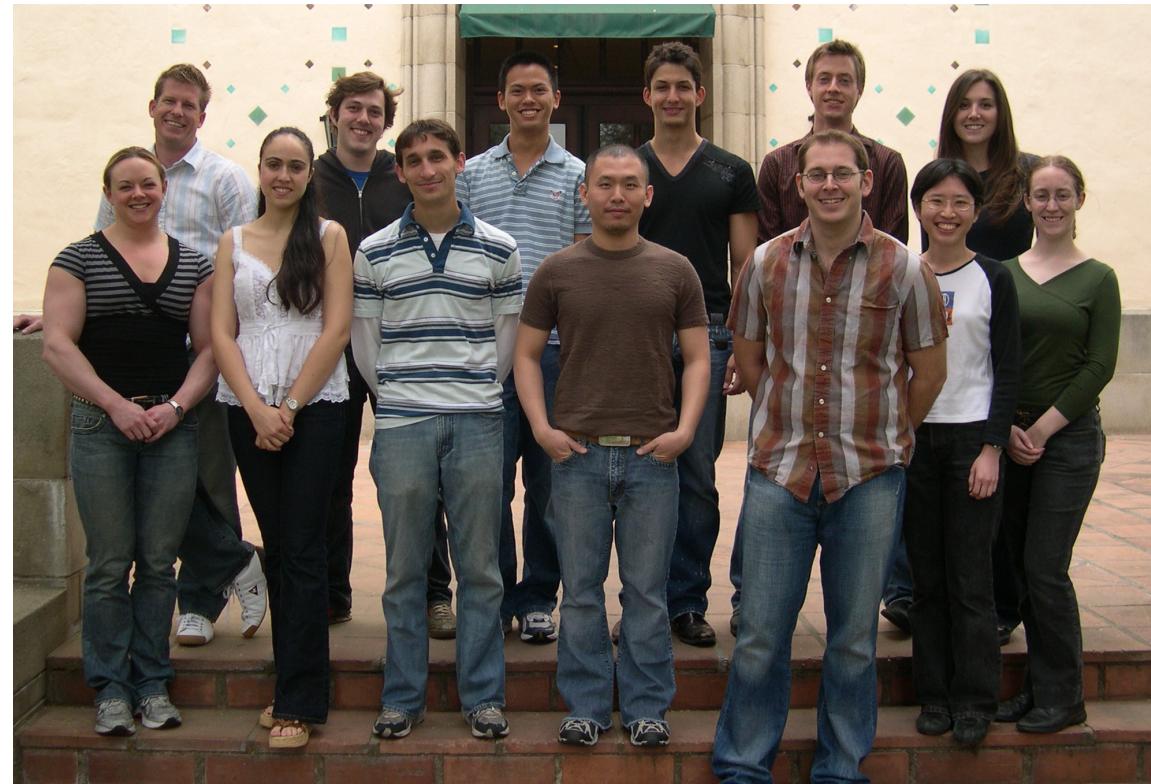
### Technicians

### **Midori Greenwood-Goodwin**

## Collaborators

The Facchini Lab (U. Calgary)

The Jensen Lab (COH)



## Funding Sources

Arnold and Mabel Beckman Foundation

Caltech

Center for Biological Circuit Design (Caltech)

City of Hope Cancer Center

Defense Advanced Research Projects Agency

Department of Defense (BCRP)

Grubstake Program (OTT Caltech)

Joseph Jacobs Institute for Molecular

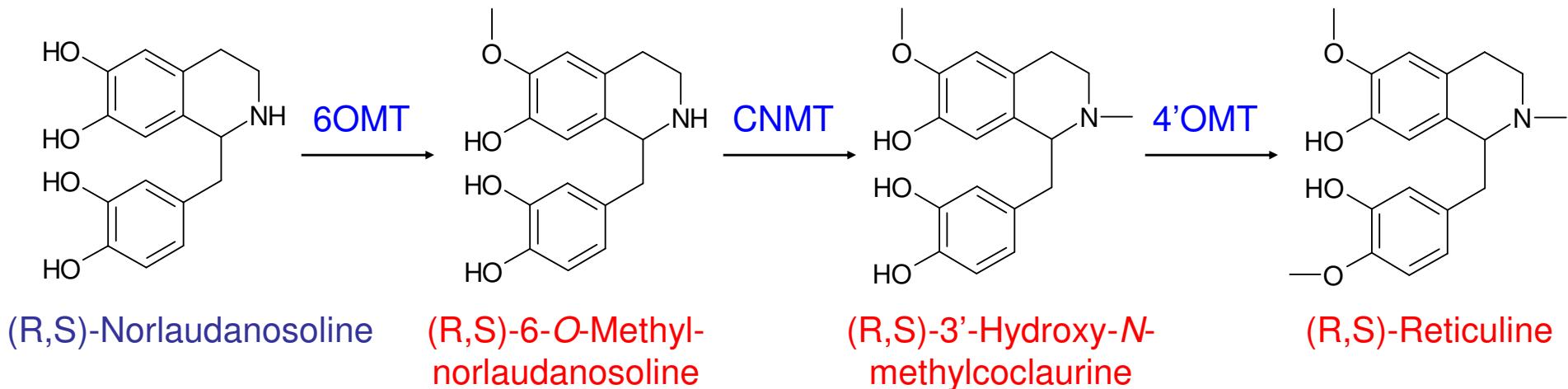
Engineering for Medicine (Caltech)

National Institutes of Health (NCI)

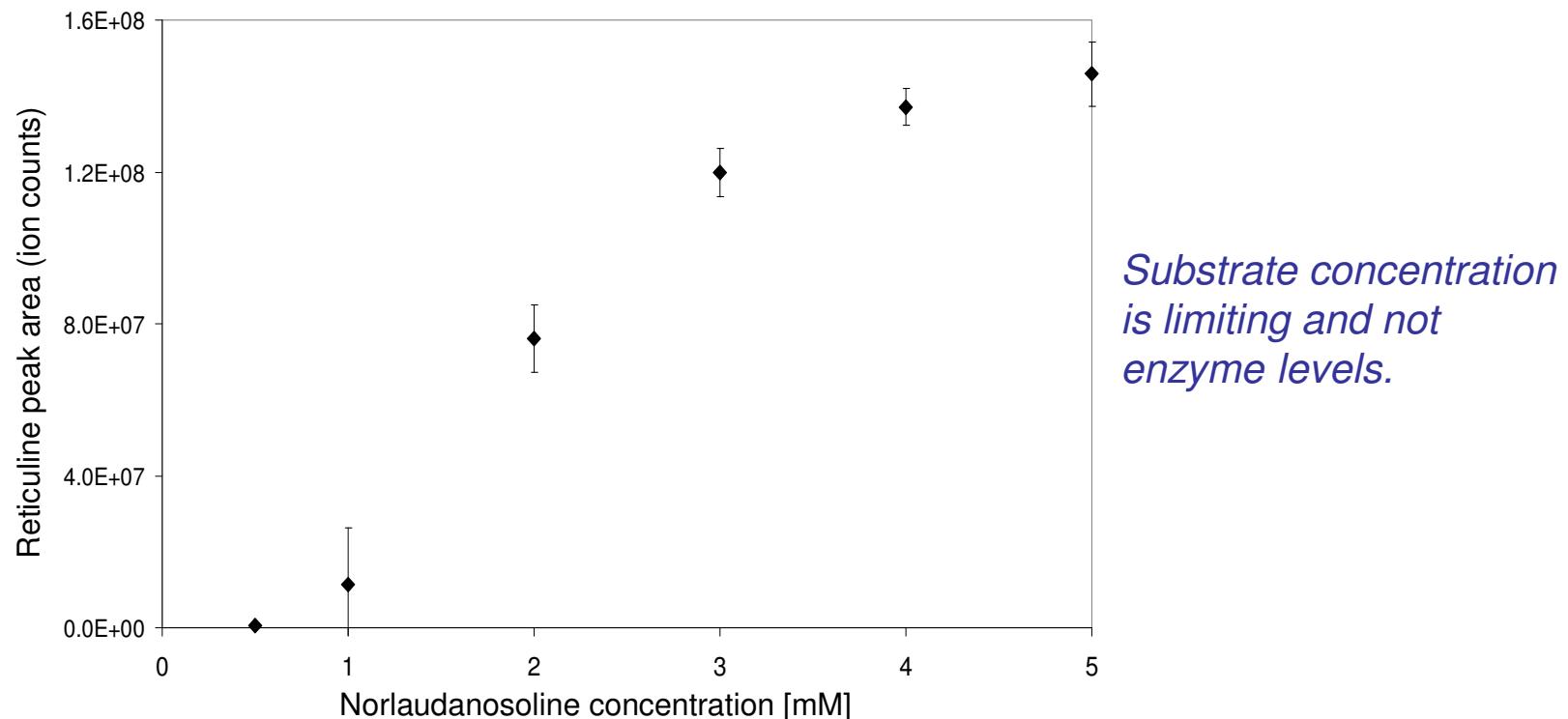
National Institutes of Health (NIGMS)

National Science Foundation (BES)

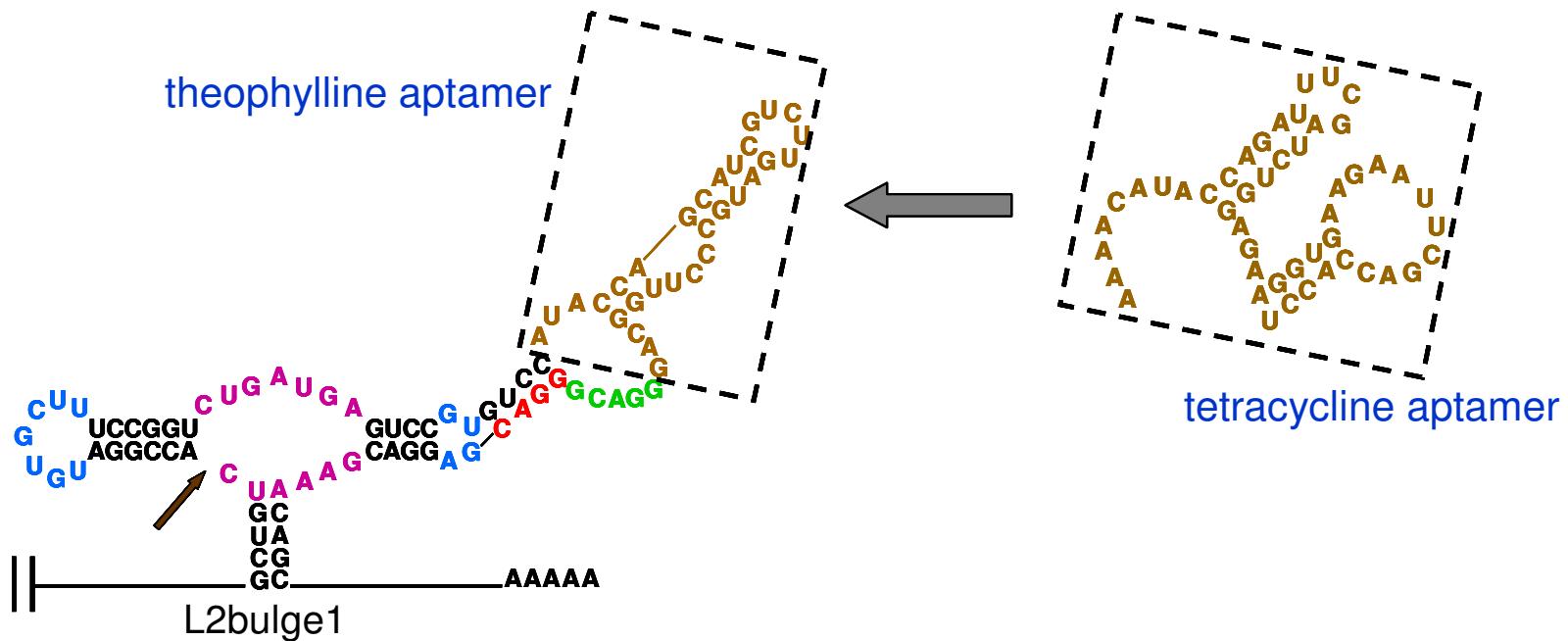
# Optimization of (R,S)-Reticuline production



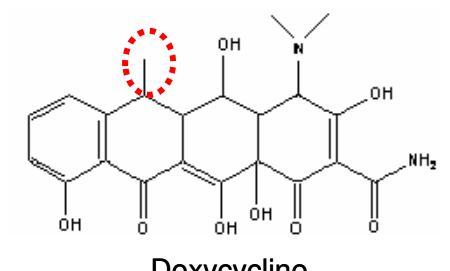
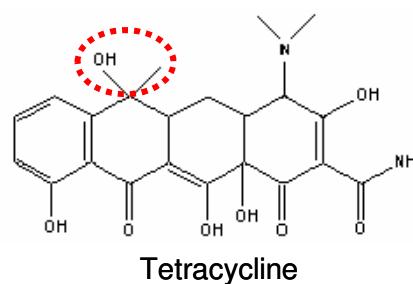
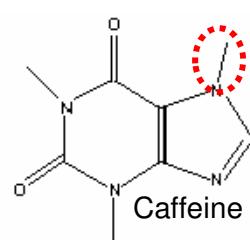
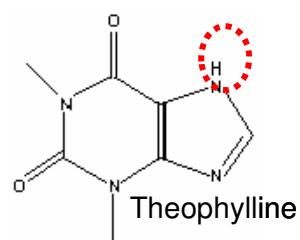
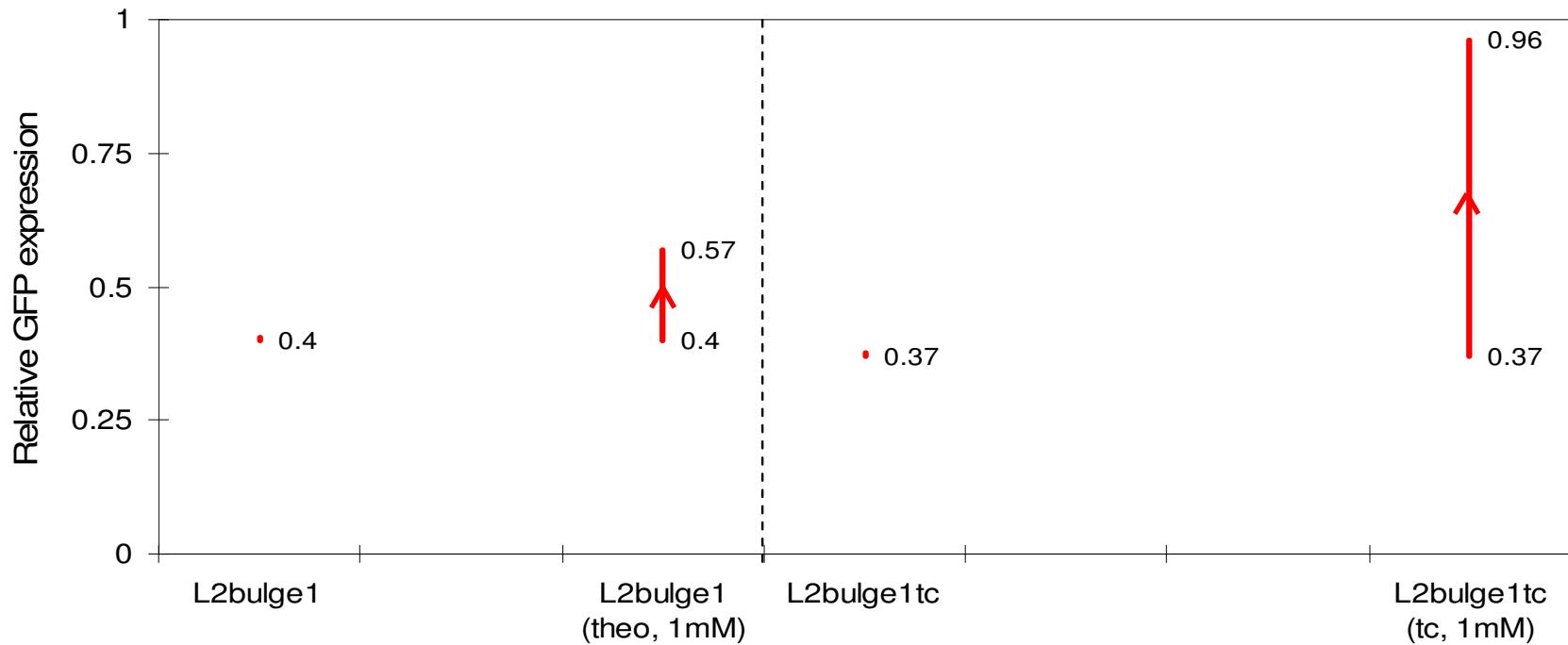
**Substrate level dependence:**



# Modularity of the sensor domain



# Modularity of the sensor domain



# Programming response properties of ribozyme switches

